



Sequence Listing

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<110> Baker, Kevin P.

Botstein, David

Desnoyers, Luc

Eaton, Dan I.

Ferrara, Napoleone

Fong, Sherman

Gao, Wei-Qiang

Goddard, Audrey

Godowski, Paul J.

Grimaldi, Christopher J.

Gurney, Austin L.

Hillan, Kenneth J.

Pan, James

Paoni, Nicholas F.

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Pro Phe Val Leu Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly
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Gln Gln Ala Glu Asn Ser Ala Val Pro Thr Ala Asp Thr Arg Ser

65 70 75

Gln Pro Arg Asp Pro Val Arg Pro Pro Arg Arg Gly Arg Gly Pro

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<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-17
<223> Signal Peptide

<220>
<221> misc_feature
<222> 36-47, 108-113, 166-171,198-203, 207-212
<223> N-myristoylation Sites.

<220>
<221> misc_feature
<222> 39-42
<223> Glycosaminoglycan Attachment Site.

<220>
<221> TRANSMEM
<222> 136-152
<223> Transmembrane Domain

<220>
<221> misc_feature

<222> 161-163, 187-190 and 253-256

<223> N-glycosylation Sites.

<400> 10

Met Leu Phe Trp Val Leu Gly Leu Leu Ile Leu Cys Gly Phe Leu

1 5 10 15

Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys

20 25 30

Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala

35 40 45

Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys

50 55 60

Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu

65 70 75

Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val

80 85 90

Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly

95 100 105

Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala

110 115 120

Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu

125 130 135

Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro

140 145 150

Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val

155 160 165

Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr Thr Pro Ser Lys

170 175 180

Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys

185 190 195

Ala Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu Phe Lys
200 205 210

Thr Asn Leu Ala Asp Pro Val Lys Val Ile Glu Lys Lys Leu Ala
215 220 225

Ile Trp Glu Gln Leu Ser Pro Asp Ile Lys Gln Gln Tyr Gly Glu
230 235 240

Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser
245 250 255

Tyr Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His
260 265 270

Ala Leu Thr Ser Leu Phe Pro Lys Thr His Tyr Ala Ala Gly Lys
275 280 285

Asp Ala Lys Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala
290 295 300

Leu Gln Asp Phe Leu Leu Leu Lys Gln Lys Ala Glu Leu Ala Asn
305 310 315

Pro Lys Ala Val

<210> 11

<211> 2720

<212> DNA

<213> Homo sapiens

<400> 11

gcgggctgtt gacggcgctg cgatggctgc ctgcgagggc aggagaagcg 50

gagctctcgg ttctctcag tcggacttcc tgacgccgcc agtgggcggg 100

gcccttggg ccgtcgccac cactgtagtc atgtaccac cgccgccgcc 150

gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200

atgacaacag caagagtgg cggcggcgct cgtgctggag gaaatggaag 250

caactgtcga gattgcagcg gaatatgatt ctcttctccc ttgcctttct 300
gcttttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350
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caccgacct gagaacttac ctgagatttc gtcacagaag acacaaagac 500
acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550
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caataccac agtggcctct tcaccacct gggcgattc acgtgggcg 1400
ccagggccga cagctactat gactacctg tgaagcagt gatccaggc 1450
gggaagcagg agacacagct gctggaagac tacgtggaag ccatcgagg 1500
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gcctgaggct ccagggtgg cttgtgtgtt tacaagctgg actcagggat 2600

cctctggcc gccccgcagg gggcttggag ggctggacgg caagtccgtc 2650

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ttgattgct ctaaccgcaa 2720

<210> 12

<211> 699

<212> PRT

<213> Homo sapiens

<220>

<221> TRANSMEM

<222> 21-40 and 84-105

<223> Transmembrane Domain (type II)

<400> 12

Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser

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Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala

20 25 30

Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro

35 40 45

His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr

50 55 60

Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp

65 70 75

Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu

80 85 90

Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala

95 100 105

Asp His Trp Lys Ala Leu Ala Phe Arg Leu Glu Glu Glu Gln Lys
110 115 120

Met Arg Pro Glu Ile Ala Gly Leu Lys Pro Ala Asn Pro Pro Val
125 130 135

Leu Pro Ala Pro Gln Lys Ala Asp Thr Asp Pro Glu Asn Leu Pro
140 145 150

Glu Ile Ser Ser Gln Lys Thr Gln Arg His Ile Gln Arg Gly Pro
155 160 165

Pro His Leu Gln Ile Arg Pro Pro Ser Gln Asp Leu Lys Asp Gly
170 175 180

Thr Gln Glu Glu Ala Thr Lys Arg Gln Glu Ala Pro Val Asp Pro
185 190 195

Arg Pro Glu Gly Asp Pro Gln Arg Thr Val Ile Ser Trp Arg Gly
200 205 210

Ala Val Ile Glu Pro Glu Gln Gly Thr Glu Leu Pro Ser Arg Arg
215 220 225

Ala Glu Val Pro Thr Lys Pro Pro Leu Pro Pro Ala Arg Thr Gln
230 235 240

Gly Thr Pro Val His Leu Asn Tyr Arg Gln Lys Gly Val Ile Asp
245 250 255

Val Phe Leu His Ala Trp Lys Gly Tyr Arg Lys Phe Ala Trp Gly
260 265 270

His Asp Glu Leu Lys Pro Val Ser Arg Ser Phe Ser Glu Trp Phe
275 280 285

Gly Leu Gly Leu Thr Leu Ile Asp Ala Leu Asp Thr Met Trp Ile
290 295 300

Leu Gly Leu Arg Lys Glu Phe Glu Glu Ala Arg Lys Trp Val Ser
305 310 315

Lys Lys Leu His Phe Glu Lys Asp Val Asp Val Asn Leu Phe Glu

320	325	330
Ser Thr Ile Arg Ile Leu Gly Gly Leu Leu Ser Ala Tyr His Leu		
335	340	345
Ser Gly Asp Ser Leu Phe Leu Arg Lys Ala Glu Asp Phe Gly Asn		
350	355	360
Arg Leu Met Pro Ala Phe Arg Thr Pro Ser Lys Ile Pro Tyr Ser		
365	370	375
Asp Val Asn Ile Gly Thr Gly Val Ala His Pro Pro Arg Trp Thr		
380	385	390
Ser Asp Ser Thr Val Ala Glu Val Thr Ser Ile Gln Leu Glu Phe		
395	400	405
Arg Glu Leu Ser Arg Leu Thr Gly Asp Lys Lys Phe Gln Glu Ala		
410	415	420
Val Glu Lys Val Thr Gln His Ile His Gly Leu Ser Gly Lys Lys		
425	430	435
Asp Gly Leu Val Pro Met Phe Ile Asn Thr His Ser Gly Leu Phe		
440	445	450
Thr His Leu Gly Val Phe Thr Leu Gly Ala Arg Ala Asp Ser Tyr		
455	460	465
Tyr Glu Tyr Leu Leu Lys Gln Trp Ile Gln Gly Gly Lys Gln Glu		
470	475	480
Thr Gln Leu Leu Glu Asp Tyr Val Glu Ala Ile Glu Gly Val Arg		
485	490	495
Thr His Leu Leu Arg His Ser Glu Pro Ser Lys Leu Thr Phe Val		
500	505	510
Gly Glu Leu Ala His Gly Arg Phe Ser Ala Lys Met Asp His Leu		
515	520	525
Val Cys Phe Leu Pro Gly Thr Leu Ala Leu Gly Val Tyr His Gly		
530	535	540

Leu Pro Ala Ser His Met Glu Leu Ala Gln Glu Leu Met Glu Thr
545 550 555

Cys Tyr Gln Met Asn Arg Gln Met Glu Thr Gly Leu Ser Pro Glu
560 565 570

Ile Val His Phe Asn Leu Tyr Pro Gln Pro Gly Arg Arg Asp Val
575 580 585

Glu Val Lys Pro Ala Asp Arg His Asn Leu Leu Arg Pro Glu Thr
590 595 600

Val Glu Ser Leu Phe Tyr Leu Tyr Arg Val Thr Gly Asp Arg Lys
605 610 615

Tyr Gln Asp Trp Gly Trp Glu Ile Leu Gln Ser Phe Ser Arg Phe
620 625 630

Thr Arg Val Pro Ser Gly Gly Tyr Ser Ser Ile Asn Asn Val Gln
635 640 645

Asp Pro Gln Lys Pro Glu Pro Arg Asp Lys Met Glu Ser Phe Phe
650 655 660

Leu Gly Glu Thr Leu Lys Tyr Leu Phe Leu Leu Phe Ser Asp Asp
665 670 675

Pro Asn Leu Leu Ser Leu Asp Ala Tyr Val Phe Asn Thr Glu Ala
680 685 690

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 13

cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 14
ccatccttct tcccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 15
gaagccttg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
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cccatgcgcc gccgcctctc cgcacgatgt tcccctcgcg gaggaagcg 100
gcgcagctgc cctgggagga cggcaggtcc ggggtgctct ccggcggcct 150
ccctcggaag tgttcgtct tccacctgtt cgtggcctgc ctctcgctgg 200
gctttctctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250
cgggcagtcg ggggacaagg gcaggagacc tcgggccctc cccgtgcctg 300
ccccccagag ccgccccctg agcactggga agaagacgca tctggggcc 350
cccaccgcct ggcagtgtg gtgcccttc gcgaacgctt cgaggagctc 400

ctggtcttcg tgccccacat gcgccgcttc ctgagcagga agaagatccg 450
gcaccacatc tacgtgtca accaggtgga ccacttcagg ttcaaccggg 500
cagcgctcat caacgtgggc ttcctggaga gcagcaacag cacggactac 550
attgccatgc acgacgtga cctgctccct ctcaacgagg agctggacta 600
tggtttcct gaggtgggc ccttcacgt ggctccccg gagtccacc 650
ctctctacca ctacaagacc tatgtcggcg gcatcctgct gctctcaag 700
cagcactacc ggtgtgcaa tgggatgtcc aaccgttct ggggtgggg 750
ccgcgaggac gacgagtct accggcgcac taaggagct gggctccagc 800
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accatgtggc tccccgact gccctgtctg tgggcggggc ccctgcact 1000
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cctactctga cctccttcac gtgccaggc ctgtgggtag tggggagggc 1450
tgaacaggac aacctctcat ccccccaaa aaaaaaaaaa aaaaaaaaaa 1500

aaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17

<211> 327

<212> PRT

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 1-42

<223> Signal peptide.

<220>

<221> misc_feature

<222> 19-25,65-71,247-253,285-291,303-310

<223> N-myristoylation site.

<220>

<221> misc_feature

<222> 27-31

<223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>

<221> TRANSMEM

<222> 29-49

<223> Transmembrane domain (type II).

<220>

<221> misc_feature

<222> 154-158

<223> N-glycosylation site.

<220>

<221> misc_feature

<222> 226-233

<223> Tyrosine kinase phosphorylation site.

<400> 17

Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp

1 5 10 15

Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser

20 25 30

Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
35 40 45

Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
50 55 60

Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
65 70 75

Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
80 85 90

Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
95 100 105

Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
110 115 120

Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
125 130 135

His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu
140 145 150

Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp
155 160 165

Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala
170 175 180

Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His
185 190 195

Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His
200 205 210

Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly
215 220 225

Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu
230 235 240

Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe

245	250	255
Arg His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg		
260	265	270
Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly		
275	280	285
Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu		
290	295	300
Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp		
305	310	315
Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser		
320	325	

<210> 18
 <211> 23
 <212> DNA
 <<213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 18
 gcgaacgctt cgaggagtcc tgg 23

<210> 19
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 19
 gcagtgcggg aagccacatg gtac 24

<210> 20
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 20

cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21

<211> 494

<212> DNA

<213> Homo sapiens

<400> 21

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gattgggcct tctttccccc ttctttctg tgtctcctgc ctcacggcc 200

tgccatgacc tgcagccaag cccagccccg tggggaaggg gagaaagtgg 250

gggatggcta agaaagctgg gagataggga acagaagagg gtagtgggtg 300

ggctaggggg gctgccttat ttaaagtggt tgttatgat tcttatacta 350

atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttc 400

cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450

taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22

<211> 73

<212> PRT

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 1-15

<223> Signal peptide.

<220>

<221> misc_feature

<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly
1 5 10 15

Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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cagcggacaa aggagcatgt ccgcgccggg gaaggcccgt cctccggccg 100

ccataaggct ccggtcgccg ctgggcccgc gccgcgtcc tgcccgccg 150

ggctccgggg cggcccgtta ggccagtgcg ccgccgtcg cccgcaggc 200

cccgcccgcc agcatggagc cccccggacg ccggcggggc cgcgcgcagc 250

cgccgtgtt gctgccgtc tcgtgttag cgctgctgc gctgtggga 300

ggcggcgccg gcggcgccgc cgcggcgctg cccgccggct gcaagcacga 350

tggcgggccc cgaggggctg gcagggcggc gggcgccgcc gagggcaagg 400

tggtgtgcag cagcctggaa ctgcgcagg tcctgcccc agatactctg 450

cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500
gaagaatggc tcattttctg ggtaagtct ccttgaaaga ttggacctcc 550
gaaacaatct tattagtagt atagatccag gtgccttctg gggactgtca 600
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ctatttacag ttaaattaga atgtccaaa tgttctgctt cgcaaaataa 2100
ccttattaaa agatttttt ttgcaggaag ataggtatta ttgcttttgc 2150
tactgtttta aagaaaacta accaggaaga actgcattac gactttcaag 2200
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acatgtgaaa aaattttatt tgacttaaaa gtttatttat ttgtttttt 2350
gtctctgatt ttaagacaat aagatgtttt catgggcccc taaaagtatc 2400
atgagccttt ggcactgcgc ctgccaagcc tagtgagaa gtcaaccctg 2450
agaccaggtg ttaatcaag caagctgtat atcaaaattt ttggcagaaa 2500
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agcaaaatga aagcattttt actgattttt aaaattggtg ctttagatat 2600
atttgactac actgtattga agcaaataga ggaggcacia ctccagcacc 2650

ctaataagaac cacatititit tcaacttagct ttctgtgggc atgtgtaatt 2700
gtattctctg cggttititaa tctcacagta ctttatttct gtcttgctcc 2750
tcaataatat cacaacaat attccagtca tttaatggc tgcataataa 2800
ctgatccaac aggtgttagg tgttctggtt tagtgtgagc actcaataaa 2850
tattgaatga atgaacgaaa aaaaaaaaaa aaa 2883

<210> 24
<211> 616
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-33
<223> Signal peptide.

<220>
<221> TRANSMEM
<222> 13-40
<223> Transmembrane domain (type II).

<400> 24
Met Glu Pro Pro Gly Arg Arg Arg Gly Arg Ala Gln Pro Pro Leu
1 5 10 15
Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly
20 25 30
Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His
35 40 45
Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
50 55 60
Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
65 70 75
Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
80 85 90

Asn Lys Ile Ser Glu Leu Lys Asn Gly Ser Phe Ser Gly Leu Ser
95 100 105

Leu Leu Glu Arg Leu Asp Leu Arg Asn Asn Leu Ile Ser Ser Ile
110 115 120

Asp Pro Gly Ala Phe Trp Gly Leu Ser Ser Leu Lys Arg Leu Asp
125 130 135

Leu Thr Asn Asn Arg Ile Gly Cys Leu Asn Ala Asp Ile Phe Arg
140 145 150

Gly Leu Thr Asn Leu Val Arg Leu Asn Leu Ser Gly Asn Leu Phe
155 160 165

Ser Ser Leu Ser Gln Gly Thr Phe Asp Tyr Leu Ala Ser Leu Arg
170 175 180

Ser Leu Glu Phe Gln Thr Glu Tyr Leu Leu Cys Asp Cys Asn Ile
185 190 195

Leu Trp Met His Arg Trp Val Lys Glu Lys Asn Ile Thr Val Arg
200 205 210

Asp Thr Arg Cys Val Tyr Pro Lys Ser Leu Gln Ala Gln Pro Val
215 220 225

Thr Gly Val Lys Gln Glu Leu Leu Thr Cys Asp Pro Pro Leu Glu
230 235 240

Leu Pro Ser Phe Tyr Met Thr Pro Ser His Arg Gln Val Val Phe
245 250 255

Glu Gly Asp Ser Leu Pro Phe Gln Cys Met Ala Ser Tyr Ile Asp
260 265 270

Gln Asp Met Gln Val Leu Trp Tyr Gln Asp Gly Arg Ile Val Glu
275 280 285

Thr Asp Glu Ser Gln Gly Ile Phe Val Glu Lys Asn Met Ile His
290 295 300

Asn Cys Ser Leu Ile Ala Ser Ala Leu Thr Ile Ser Asn Ile Gln

305	310	315
Ala Gly Ser Thr Gly Asn Trp Gly Cys His Val Gln Thr Lys Arg		
320	325	330
Gly Asn Asn Thr Arg Thr Val Asp Ile Val Val Leu Glu Ser Ser		
335	340	345
Ala Gln Tyr Cys Pro Pro Glu Arg Val Val Asn Asn Lys Gly Asp		
350	355	360
Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr Ala Tyr Leu Gln		
365	370	375
Cys Thr Arg Asn Thr His Gly Ser Gly Ile Tyr Pro Gly Asn Pro		
380	385	390
Gln Asp Glu Arg Lys Ala Trp Arg Arg Cys Asp Arg Gly Gly Phe		
395	400	405
Trp Ala Asp Asp Asp Tyr Ser Arg Cys Gln Tyr Ala Asn Asp Val		
410	415	420
Thr Arg Val Leu Tyr Met Phe Asn Gln Met Pro Leu Asn Leu Thr		
425	430	435
Asn Ala Val Ala Thr Ala Arg Gln Leu Leu Ala Tyr Thr Val Glu		
440	445	450
Ala Ala Asn Phe Ser Asp Lys Met Asp Val Ile Phe Val Ala Glu		
455	460	465
Met Ile Glu Lys Phe Gly Arg Phe Thr Lys Glu Glu Lys Ser Lys		
470	475	480
Glu Leu Gly Asp Val Met Val Asp Ile Ala Ser Asn Ile Met Leu		
485	490	495
Ala Asp Glu Arg Val Leu Trp Leu Ala Gln Arg Glu Ala Lys Ala		
500	505	510
Cys Ser Arg Ile Val Gln Cys Leu Gln Arg Ile Ala Thr Tyr Arg		
515	520	525

Leu Ala Gly Gly Ala His Val Tyr Ser Thr Tyr Ser Pro Asn Ile
530 535 540

Ala Leu Glu Ala Tyr Val Ile Lys Ser Thr Gly Phe Thr Gly Met
545 550 555

Thr Cys Thr Val Phe Gln Lys Val Ala Ala Ser Asp Arg Thr Gly
560 565 570

Leu Ser Asp Tyr Gly Arg Arg Asp Pro Glu Gly Asn Leu Asp Lys
575 580 585

Gln Leu Ser Phe Lys Cys Asn Val Ser Asn Thr Phe Ser Ser Leu
590 595 600

Ala Leu Lys Val Cys Tyr Ile Leu Gln Ser Phe Lys Thr Ile Tyr
605 610 615

Ser

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 25

gaggactcac caatctggtt cggc 24

<210> 26

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 26

aactggaaag gaaggctgtc tccc 24

<210> 27
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 27
gtaaaggaga agaacatcac ggtacgggat accaggtgtg ttatcctaa 50

<210> 28
<211> 683
<212> DNA
<213> Homo sapiens

<400> 28
gcgtggggat gtctaggagc tcgaaggtgg tgctgggcct ctcggtgctg 50
ctgacggcgg ccacagtggc cggcgtacat gtgaagcagc agtgggacca 100
gcagaggctt cgtgacggag ttatcagaga cattgagagg caaatcgga 150
aaaaagaaaa cattcgtctt ttgggagaac agattatctt gactgagcaa 200
cttgaagcag aaagagagaa gatgttattg gcaaaaggat ctcaaaaatc 250
atgacttgaa tgtgaaatat ctgttgaca gacaacacga gtttgtgtgt 300
gtgtgttgat ggagagtagc ttagtagtat cttcatcttt tttttggtc 350
actgtccttt taaacttgat caaataaagg acagtgggtc atataagtta 400
ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450
tttgaagag tctgtctggg tgatcctggt agaagcccca ttaggtcac 500
tgtccagtgc ttagggttgt tactgagaag cactgccgag cttgtgagaa 550
ggaagggatg gatagtagca tccacctgag tagtctgac agtcggcatg 600
atgacgaagc cagagaaca tcgacctcag aaggactgga ggaagtgaa 650

gtggaggag agacgtcct gatcgtcgaa tcc 683

<210> 29

<211> 81

<212> PRT

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 1-21

<223> Signal peptide.

<400> 29

Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu

1 5 10 15

Thr Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp

20 25 30

Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln

35 40 45

Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile

50 55 60

Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala

65 70 75

Lys Gly Ser Gln Lys Ser

80

<210> 30

<211> 2128

<212> DNA

<213> Homo sapiens

<400> 30

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tacagcctgt tccaagtgtg gcttaatccg tctccaccac cagatctttc 100

tccgtggatt cctctgctaa gaccgtgcc atgccagtga cggtaacccg 150

caccaccatc acaaccacca cgacgtcatc ttggggcctg gggccccca 200
tgatcgtggg gtccccctgg gccctgacac agccccctggg tctccttcgc 250
ctgctgcagc tgggtcttac ctgcgtggcc ttctcgtgg tggttagcgt 300
ggggcgctgg acgggggtcca tgggcaactg gtccatgttc acctggtgct 350
tctgtttctc cgtgaccctg atcatcctca tctgggagct gtgcgggctc 400
cagggcccgt tccccctgc ttggcgcaac ttccccatca cttcgcctg 450
ctatcgggcc ctcttctgcc tctcggectc catcatctac cccaccacct 500
atgtccagtt cctgtccac ggccgttcgc gggaccacgc catcgccgc 550
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acctggggga gtgcaccaac gtgtacca tccccctccc cagcttcctg 850
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cagccttgcc agagattggc tccagaattt ttgccaggct tacagaacac 2050
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<210> 31

<211> 322

<212> PRT

<213> Homo sapiens

<400> 31

Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Thr

1 5 10 15

Ser Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly Ser Pro Arg
20 25 30

Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val
35 40 45

Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
50 55 60

Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
65 70 75

Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
80 85 90

Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
95 100 105

Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr
110 115 120

Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
125 130 135

His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala
140 145 150

Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile
155 160 165

Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu
170 175 180

Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn
185 190 195

Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr
200 205 210

Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu
215 220 225

Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu
230 235 240

Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu
245 250 255

Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln
260 265 270

Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr
275 280 285

Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr
290 295 300

Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala
305 310 315

His Leu Val Phe Val Lys Val
320

<210> 32

<211> 3680

<212> DNA

<213> Homo sapiens

<400> 32

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tttcacatg ttggccaggc tggcttgaa ctcgtgacct catgatccgc 100

tcacctggc ctccaaagt gctgggatta caggcatgag ccactgacgc 150

ctggccagcc tatgcatttt taagaaatta ttctgtatta ggtgctgtgc 200

taaacattgg gcactacagt gacaaaaa gactgaattc cccaagagcc 250

aaagaccagt gagggagacc aacaagaaac aggaaatgca aaagagacca 300

ttattactca ctatgactaa gggtcacaaa tggggtacgt tgatggagag 350

tgatttgta agagactaca gagggaggac agactacaa gaggggggcc 400

aggaaagctc ctctgacgag gtggtatttc agcccaaact ggaagaatga 450
gaaagagcta gccagccatc agaatagtcc agaagagatg gggagcacta 500
cactcactac actttggcct gagaaaatag catgggattg gaggaggctg 550
ggggaacacc acttctgccg acctgggcag gaggcattga gggcttgaga 600
aaggggcaatg gcagtagcag tagaaaggac agggtaggag cagggacttt 650
gcaggtggaa tcattaggtc ttatcaacag atatgggcaa gcaaagccag 700
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taatataaaa atctttgtaa atctctaaaa 3680

<210> 33
<211> 335
<212> PRT
<213> Homo sapiens

<400> 33
Met Phe Leu Ala Thr Leu Ser Phe Leu Leu Pro Phe Ala His Pro
1 5 10 15

Phe Gly Thr Val Ser Cys Glu Tyr Met Leu Gly Ser Pro Leu Ser
20 25 30

Ser Leu Ala Gln Val Asn Leu Ser Pro Phe Ser His Pro Lys Val
35 40 45

His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu
50 55 60

Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu
65 70 75

Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro
80 85 90

Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys
95 100 105

Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala
110 115 120

Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg
125 130 135

Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys
140 145 150

Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp
155 160 165

Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala
170 175 180

Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly

185	190	195
His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu		
200	205	210
Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser		
215	220	225
Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu		
230	235	240
Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro		
245	250	255
Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala		
260	265	270
Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser		
275	280	285
Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu		
290	295	300
Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser		
305	310	315
Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala		
320	325	330
Glu Pro Glu Glu Gln		
335		

<210> 34

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

tgtccttgt cccagacttc tgtcc 25

<210> 35

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 35

ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcgatgct 50

<210> 36

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 36

ttccactcaa tgaggtgagc cactc 25

<210> 37

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 37

ggcgagccct aactatccag gag 23

<210> 38

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 38

ggagatcgct gcgctggcca ggtcctccct gcatggat 39

<210> 39

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 39

ctgctgcaaa gcgagcctct tg 22

<210> 40

<211> 2084

<212> DNA

<213> Homo sapiens

<400> 40

ggttcctggg cgctctgtta cacaagcaag atacagccag cccacctaa 50

ttttgttcc ctggcaccct cctgctcagt gcgacattgt cacacttaac 100

ccatctgttt tctctaagc acgacagatt cctttcagac aggacaactg 150

tgatattca gttcctgatt gtaaatacct cctaagcctg aagcttctgt 200

tactagccat tgtgagcttc agtttttca tctgcaaaat gggcataata 250

caatctatc ttgccacatc aagggattgt tattccttta aaaaaaaccc 300

aataccaaag aagcctacaa tgttggcctt agccaaaatt ctgttgattt 350

caacgttgtt ttattcactt ctatcgggga gccatggaaa agaaaatcaa 400

gacataaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450

taaacctatt tctttggaaa gtgaagcaaa cttaaactca gataaagaaa 500

atataaccac ctcaaattc aaggcgagtc attccctcc tttgaatcta 550

cccaacaaca gccacggaat aacagatttc tccagtaact catcagcaga 600

gcattctttg ggcagictaa aaccacatc taccattcc acaagcctc 650

ccttgatcca tagctttgtt tctaaagtgc ctggaatgc acctatagca 700
gatgaagatc ttgtcccat ctcagacat cccaatgta cacctgctct 750
gtcttcagaa aacttcactt ggtctttggt caatgacacc gtgaaaactc 800
ctgataacag ttccattaca gttagcatcc tctcttcaga accaacttct 850
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catagcccag agtttctgtt attgggaaat tgaggcaata gaaatgacag 1850

acctgtattc tagtacgtta taattttcta gatcagcaca cacatgatca 1900

gcccactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950

aggaaagctg accctacca ggaaagtaat agcttcttta aaagtcttca 2000

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<210> 41

<211> 334

<212> PRT

<213> Homo sapiens

<400> 41

Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr

1 5 10 15

Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn

20 25 30

Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys

35 40 45

Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu

50 55 60

Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu

65 70 75

Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn

80 85 90

Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr

95 100 105

Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val

110 115 120

Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
125 130 135

Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
140 145 150

Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
155 160 165

Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
170 175 180

Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
185 190 195

Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu
200 205 210

Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn
215 220 225

Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe
230 235 240

Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu
245 250 255

Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser
260 265 270

His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu
275 280 285

Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser
290 295 300

Tyr Tyr Asn Pro Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu
305 310 315

Glu Asn Ala Arg Asp Gly Ile Pro Met Asp Asp Ile Pro Pro Leu
320 325 330

Arg Thr Ser Val

<210> 42
<211> 1594
<212> DNA
<213> Homo sapiens

<400> 42
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cccctaccgc cgtgcaaaaag gaggaggcgc ggcaagacgt ggaggccctc 150

ctgagccgca cggtcagaac tcagatactg accggcaagg agtccgagt 200

tgccaccag gaaaaagagg gctcctctgg gagatgtatg cttactctct 250

taggccttc attcatcttg gcaggactta ttgttggtgg agcctgcatt 300

tacaagtact tcatgccaa gagcaccatt taccgtggag agatgtgctt 350

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tattcatgac ttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550

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aatctggtag agctctttgg caaactggcg agtggcagat atctgcctca 650

aacctatgtg gtcgagaag acctagtgc tgtggaggaa attcgtgatg 700

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 ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu

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Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg

20 25 30

Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu

35 40 45

Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu
50 55 60

Ser Phe Ile Leu Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr
65 70 75

Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met Cys
80 85 90

Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu
95 100 105

Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp
110 115 120

Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp
125 130 135

Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr
140 145 150

Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys Tyr Leu Met Pro Leu
155 160 165

Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe
170 175 180

Gly Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val
185 190 195

Arg Glu Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn
200 205 210

Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe
215 220 225

Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala
230 235 240

Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile
245 250 255

Val Glu Thr Lys Ile Cys Gln Glu

<210> 44

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 44

gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 45

gggaactgct atctgatgcc 20

<210> 46

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

caggatctcc tcttgcatgc tgcagc 26

<210> 47

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 47
cttctcgaac cacataagtt tgaggcag 28

<210> 48
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
cacgattccc tccacagcaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

<400> 49
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gttccggcgg cagccccag cctcctcacc ctctgttg gcgtgctggg 200
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ggcaggaggt cctctcccc atccctccat ctggggctcc cccaacctct 1850

gcacagctct ccaggtgctg agatataatg caccagcaca ataaccttt 1900

attccggcct gaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1950

aaaaaaaaa aaaaaaaga 1969

<210> 50
 <211> 283
 <212> PRT
 <213> Homo sapiens

<400> 50
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Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu
 20 25 30

Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
 35 40 45

Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
 50 55 60

Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
 65 70 75

Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe
 80 85 90

Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala
 95 100 105

Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln
 110 115 120

Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys

125	130	135
Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe		
140	145	150
Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala		
155	160	165
Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr		
170	175	180
Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Gly Asp		
185	190	195
Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu Glu Lys		
200	205	210
Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro		
215	220	225
Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu		
230	235	240
Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly		
245	250	255
Ser Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro		
260	265	270
Glu Ser Pro Cys Ala Cys Ser Ser Val His Pro Ser Val		
275	280	

<210> 51

<211> 1734

<212> DNA

<213> Homo sapiens

<400> 51

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gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga 150

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<210> 52
 <211> 440
 <212> PRT
 <213> Homo sapiens

<400> 52
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 20 25 30
 Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
 35 40 45
 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly
 50 55 60
 Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr
 65 70 75
 Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly
 80 85 90

Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala
95 100 105

Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val
110 115 120

Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val
125 130 135

Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile
140 145 150

Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro
155 160 165

Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser
170 175 180

Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln
185 190 195

Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly
200 205 210

Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln
215 220 225

Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly
230 235 240

Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser
245 250 255

Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly
260 265 270

Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser
275 280 285

Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Asn Ser Gly Gly Ser
290 295 300

Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly

305	310	315
Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly Asn Gly His		
320	325	330
Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly		
335	340	345
Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn		
350	355	360
Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser		
365	370	375
Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly		
380	385	390
Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser		
395	400	405
Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser		
410	415	420
Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg		
425	430	435
Ser Ser Arg Ile Pro		
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<210> 53
 <211> 3580
 <212> DNA
 <213> Homo sapiens

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<210> 54

<211> 280

<212> PRT

<213> Homo sapiens

<400> 54

Met Cys Phe Leu Asn Lys Leu Leu Leu Leu Ala Val Leu Gly Trp

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Leu Phe Gln Ile Pro Thr Val Pro Glu Asp Leu Phe Phe Leu Glu

20 25 30

Glu Gly Pro Ser Tyr Ala Phe Glu Val Asp Thr Val Ala Pro Glu

35 40 45

His Gly Leu Asp Asn Ala Pro Val Val Asp Gln Gln Leu Leu Tyr

50 55 60

Thr Cys Cys Pro Tyr Ile Gly Glu Leu Arg Lys Leu Leu Ala Ser

65 70 75

Trp Val Ser Gly Ser Ser Gly Arg Ser Gly Gly Phe Met Arg Lys

80 85 90

Ile Thr Pro Thr Thr Thr Thr Ser Leu Gly Ala Gln Pro Ser Gln

95 100 105

Thr Ser Gln Gly Leu Gln Ala Gln Leu Ala Gln Ala Phe Phe His

110 115 120

Asn Gln Pro Pro Ser Leu Arg Arg Thr Val Glu Phe Val Ala Glu

125 130 135

Arg Ile Gly Ser Asn Cys Val Lys His Ile Lys Ala Thr Leu Val

140 145 150

Ala Asp Leu Val Arg Gln Ala Glu Ser Leu Leu Gln Glu Gln Leu

155 160 165

Val Thr Gln Gly Glu Glu Gly Gly Asp Pro Ala Gln Leu Leu Glu
170 175 180

Ile Leu Cys Ser Gln Leu Cys Pro His Gly Ala Gln Ala Leu Ala
185 190 195

Leu Gly Arg Glu Phe Cys Gln Arg Lys Ser Pro Gly Ala Val Arg
200 205 210

Ala Leu Leu Pro Glu Glu Thr Pro Ala Ala Val Leu Ser Ser Ala
215 220 225

Glu Asn Ile Ala Val Gly Leu Ala Thr Glu Lys Ala Cys Ala Trp
230 235 240

Leu Ser Ala Asn Ile Thr Ala Leu Ile Arg Arg Glu Val Lys Ala
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Ala Val Ser Arg Thr Leu Arg Ala Gln Gly Pro Glu Pro Ala Ala
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Arg Gly Glu Arg Arg Gly Cys Ser Arg Ala
275 280

<210> 55

<211> 2401

<212> DNA

<213> Homo sapiens

<400> 55

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cgacacctac ccctcagcag acgccggaga gaaatgagta gcaacaaaga 200

gcagcgggtca gcagtgttcg tgatcctctt tgcctcctc accatcctca 250

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<210> 56
<211> 299
<212> PRT

<213> Homo sapiens

<400> 56

Met Ser Ser Asn Lys Glu Gln Arg Ser Ala Val Phe Val Ile Leu
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Phe Ala Leu Ile Thr Ile Leu Ile Leu Tyr Ser Ser Asn Ser Ala
20 25 30

Asn Glu Val Phe His Tyr Gly Ser Leu Arg Gly Arg Ser Arg Arg
35 40 45

Pro Val Asn Leu Lys Lys Trp Ser Ile Thr Asp Gly Tyr Val Pro
50 55 60

Ile Leu Gly Asn Lys Thr Leu Pro Ser Arg Cys His Gln Cys Val
65 70 75

Ile Val Ser Ser Ser Ser His Leu Leu Gly Thr Lys Leu Gly Pro
80 85 90

Glu Ile Glu Arg Ala Glu Cys Thr Ile Arg Met Asn Asp Ala Pro
95 100 105

Thr Thr Gly Tyr Ser Ala Asp Val Gly Asn Lys Thr Thr Tyr Arg
110 115 120

Val Val Ala His Ser Ser Val Phe Arg Val Leu Arg Arg Pro Gln
125 130 135

Glu Phe Val Asn Arg Thr Pro Glu Thr Val Phe Ile Phe Trp Gly
140 145 150

Pro Pro Ser Lys Met Gln Lys Pro Gln Gly Ser Leu Val Arg Val
155 160 165

Ile Gln Arg Ala Gly Leu Val Phe Pro Asn Met Glu Ala Tyr Ala
170 175 180

Val Ser Pro Gly Arg Met Arg Gln Phe Asp Asp Leu Phe Arg Gly
185 190 195

Glu Thr Gly Lys Asp Arg Glu Lys Ser His Ser Trp Leu Ser Thr

200	205	210
Gly Trp Phe Thr Met Val Ile Ala Val Glu Leu Cys Asp His Val		
215	220	225
His Val Tyr Gly Met Val Pro Pro Asn Tyr Cys Ser Gln Arg Pro		
230	235	240
Arg Leu Gln Arg Met Pro Tyr His Tyr Tyr Glu Pro Lys Gly Pro		
245	250	255
Asp Glu Cys Val Thr Tyr Ile Gln Asn Glu His Ser Arg Lys Gly		
260	265	270
Asn His His Arg Phe Ile Thr Glu Lys Arg Val Phe Ser Ser Trp		
275	280	285
Ala Gln Leu Tyr Gly Ile Thr Phe Ser His Pro Ser Trp Thr		
290	295	

<210> 57

<211> 4277

<212> DNA

<213> Homo sapiens

<400> 57

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gaagtcttgt cgacatttat accgtctgag ggtagcagct cgaaactaga 250

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<210> 58

<211> 1115

<212> PRT

<213> Homo sapiens

<400> 58

Met Leu Arg Gly Thr Met Thr Ala Trp Arg Gly Met Arg Pro Glu

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Val Thr Leu Ala Cys Leu Leu Leu Ala Thr Ala Gly Cys Phe Ala

20 25 30

Asp Leu Asn Glu Val Pro Gln Val Thr Val Gln Pro Ala Ser Thr

35 40 45

Val Gln Lys Pro Gly Gly Thr Val Ile Leu Gly Cys Val Val Glu

50 55 60

Pro Pro Arg Met Asn Val Thr Trp Arg Leu Asn Gly Lys Glu Leu

65 70 75

Asn Gly Ser Asp Asp Ala Leu Gly Val Leu Ile Thr His Gly Thr
80 85 90

Leu Val Ile Thr Ala Leu Asn Asn His Thr Val Gly Arg Tyr Gln
95 100 105

Cys Val Ala Arg Met Pro Ala Gly Ala Val Ala Ser Val Pro Ala
110 115 120

Thr Val Thr Leu Ala Asn Leu Gln Asp Phe Lys Leu Asp Val Gln
125 130 135

His Val Ile Glu Val Asp Glu Gly Asn Thr Ala Val Ile Ala Cys
140 145 150

His Leu Pro Glu Ser His Pro Lys Ala Gln Val Arg Tyr Ser Val
155 160 165

Lys Gln Glu Trp Leu Glu Ala Ser Arg Gly Asn Tyr Leu Ile Met
170 175 180

Pro Ser Gly Asn Leu Gln Ile Val Asn Ala Ser Gln Glu Asp Glu
185 190 195

Gly Met Tyr Lys Cys Ala Ala Tyr Asn Pro Val Thr Gln Glu Val
200 205 210

Lys Thr Ser Gly Ser Ser Asp Arg Leu Arg Val Arg Arg Ser Thr
215 220 225

Ala Glu Ala Ala Arg Ile Ile Tyr Pro Pro Glu Ala Gln Thr Ile
230 235 240

Ile Val Thr Lys Gly Gln Ser Leu Ile Leu Glu Cys Val Ala Ser
245 250 255

Gly Ile Pro Pro Pro Arg Val Thr Trp Ala Lys Asp Gly Ser Ser
260 265 270

Val Thr Gly Tyr Asn Lys Thr Arg Phe Leu Leu Ser Asn Leu Leu
275 280 285

Ile Asp Thr Thr Ser Glu Glu Asp Ser Gly Thr Tyr Arg Cys Met

290	295	300
Ala Asp Asn Gly Val Gly Gln Pro Gly Ala Ala Val Ile Leu Tyr		
305	310	315
Asn Val Gln Val Phe Glu Pro Pro Glu Val Thr Met Glu Leu Ser		
320	325	330
Gln Leu Val Ile Pro Trp Gly Gln Ser Ala Lys Leu Thr Cys Glu		
335	340	345
Val Arg Gly Asn Pro Pro Pro Ser Val Leu Trp Leu Arg Asn Ala		
350	355	360
Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala		
365	370	375
Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln		
380	385	390
Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln		
395	400	405
Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp		
410	415	420
Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu		
425	430	435
Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg		
440	445	450
Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu		
455	460	465
Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser		
470	475	480
Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro		
485	490	495
Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val		
500	505	510

Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile
515 520 525

Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu
530 535 540

Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys
545 550 555

Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg
560 565 570

Arg Pro Lys Pro Glu Ile Met Ala Ser Lys Glu Gln Gln Ile Gln
575 580 585

Arg Asp Asp Pro Gly Ala Ser Pro Gln Ser Ser Ser Gln Pro Asp
590 595 600

His Gly Arg Leu Ser Pro Pro Glu Ala Pro Asp Arg Pro Thr Ile
605 610 615

Ser Thr Ala Ser Glu Thr Ser Val Tyr Val Thr Trp Ile Pro Arg
620 625 630

Gly Asn Gly Gly Phe Pro Ile Gln Ser Phe Arg Val Glu Tyr Lys
635 640 645

Lys Leu Lys Lys Val Gly Asp Trp Ile Leu Ala Thr Ser Ala Ile
650 655 660

Pro Pro Ser Arg Leu Ser Val Glu Ile Thr Gly Leu Glu Lys Gly
665 670 675

Thr Ser Tyr Lys Phe Arg Val Arg Ala Leu Asn Met Leu Gly Glu
680 685 690

Ser Glu Pro Ser Ala Pro Ser Arg Pro Tyr Val Val Ser Gly Tyr
695 700 705

Ser Gly Arg Val Tyr Glu Arg Pro Val Ala Gly Pro Tyr Ile Thr
710 715 720

Phe Thr Asp Ala Val Asn Glu Thr Thr Ile Met Leu Lys Trp Met

725	730	735
Tyr Ile Pro Ala Ser Asn Asn Asn Thr Pro Ile His Gly Phe Tyr		
740	745	750
Ile Tyr Tyr Arg Pro Thr Asp Ser Asp Asn Asp Ser Asp Tyr Lys		
755	760	765
Lys Asp Met Val Glu Gly Asp Lys Tyr Trp His Ser Ile Ser His		
770	775	780
Leu Gln Pro Glu Thr Ser Tyr Asp Ile Lys Met Gln Cys Phe Asn		
785	790	795
Glu Gly Gly Glu Ser Glu Phe Ser Asn Val Met Ile Cys Glu Thr		
800	805	810
Lys Ala Arg Lys Ser Ser Gly Gln Pro Gly Arg Leu Pro Pro Pro		
815	820	825
Thr Leu Ala Pro Pro Gln Pro Pro Leu Pro Glu Thr Ile Glu Arg		
830	835	840
Pro Val Gly Thr Gly Ala Met Val Ala Arg Ser Ser Asp Leu Pro		
845	850	855
Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile Ile		
860	865	870
Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln		
875	880	885
Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro		
890	895	900
Ser Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His		
905	910	915
Gln Ala Ser Gly Gln Pro Tyr Leu Ser Gly Ile Ser Gly Arg Ala		
920	925	930
Cys Ala Asn Gly Ile His Met Asn Arg Gly Cys Pro Ser Ala Ala		
935	940	945

Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu
950 955 960

Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His
965 970 975

Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly
980 985 990

Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro
995 1000 1005

Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys
1010 1015 1020

Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg
1025 1030 1035

Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro
1040 1045 1050

Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu
1055 1060 1065

Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp
1070 1075 1080

Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly
1085 1090 1095

Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr
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Pro Pro Leu Thr Ile
1115

<210> 59

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 59

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<210> 60

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

gcacacgtag cctgtcgctg gaggc 24

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 61

caccccaaag ccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62

<211> 1661

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 678

<223> unknown base

<400> 62

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tgctgacaca gtcggtcccc gcagaggtca ctgtggcaaa gcctcacaaa 1600

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cacatggaaa a 1661

<210> 63

<211> 487

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 196, 386

<223> unknown amino acid

<400> 63

Met Gln Pro Thr Gly Arg Glu Gly Ser Arg Ala Leu Ser Arg Arg

1 5 10 15

Tyr Leu Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Arg

20 25 30

Gln Pro Val Thr Arg Ala Glu Thr Thr Pro Gly Ala Pro Arg Ala

35 40 45

Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val

50 55 60

Pro Ser Ala Leu Thr Thr Pro Gly Leu Thr Thr Pro Gly Thr Pro

65 70 75

Lys Thr Leu Asp Leu Arg Gly Arg Ala Gln Ala Leu Met Arg Ser

80	85	90
Phe Pro Leu Val Asp Gly His Asn Asp Leu Pro Gln Val Leu Arg		
95	100	105
Gln Arg Tyr Lys Asn Val Leu Gln Asp Val Asn Leu Arg Asn Phe		
110	115	120
Ser His Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val		
125	130	135
Gly Ala Gln Phe Trp Ser Ala Ser Val Ser Cys Gln Ser Gln Asp		
140	145	150
Gln Thr Ala Val Arg Leu Ala Leu Glu Gln Ile Asp Leu Ile His		
155	160	165
Arg Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala		
170	175	180
Glu Gly Leu Asn Ser Ser Gln Lys Leu Ala Cys Leu Ile Gly Val		
185	190	195
Xaa Gly Gly His Ser Leu Asp Ser Ser Leu Ser Val Leu Arg Ser		
200	205	210
Phe Tyr Val Leu Gly Val Arg Tyr Leu Thr Leu Thr Phe Thr Cys		
215	220	225
Ser Thr Pro Trp Ala Glu Ser Ser Thr Lys Phe Arg His His Met		
230	235	240
Tyr Thr Asn Val Ser Gly Leu Thr Ser Phe Gly Glu Lys Val Val		
245	250	255
Glu Glu Leu Asn Arg Leu Gly Met Met Ile Asp Leu Ser Tyr Ala		
260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro		
275	280	285
Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu		
290	295	300

Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly
305 310 315

Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu
320 325 330

Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg
335 340 345

Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp
350 355 360

Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr
365 370 375

Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu
380 385 390

Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg
395 400 405

Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val
410 415 420

Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser
425 430 435

His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val
440 445 450

Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala
455 460 465

Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro
470 475 480

Thr Phe Thr Gln Trp Leu Cys
485

<210> 64

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 65

gtcacacaca gctctggcag ctgag 25

<210> 66

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

tgctaggctc tgcccacaa tgcacccgag agcaggagct gaaagcctct 50

aacaccaca gatecctcta tgactgcaat gtgaggtgtc cggtttgtct 100

ggcccagcaa gcctgataag catgaagctc ttatctttgg tggctgtggt 150

cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200

tccggtgcaa atgcatctgt ccacctata gaaacatcag tgggcacatt 250

tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300
gcccattgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350
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ttttatttct ctca 1564

<210> 68

<211> 183

<212> PRT

<213> Homo sapiens

<400> 68

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
1 5 10 15

Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
20 25 30

Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
35 40 45

Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
50 55 60

Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu
65 70 75

Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val
80 85 90

Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr
95 100 105

Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp
110 115 120

Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala
125 130 135

Arg Ser Met Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
140 145 150

Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys
155 160 165

Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys
170 175 180

Met Leu Ser

<210> 69

<211> 3170

<212> DNA

<213> Homo sapiens

<400> 69

agcgggtctc gcttgggttc cgctaatttc tgcctgagg cgtgagactg 50

agttcatagg gtctgggtc cccgaaccag gaagggtga gggaacacaa 100

tctgcaagcc cccgcgaccc aagtgagggg ccccggttg gggtcctccc 150

tccctttgca ttccacccc tccgggcttt gcgtcttct ggggaccccc 200

tcgccgggag atggccgct tgatgcggag caaggattcg tctgctgcc 250

tgctctact ggccgcggtg ctgatggtg agagtcaca gatcggcagt 300

tcggggcca aactcaact catcaagtc tctctgggcg gggagacgcc 350

tggtcaggcc gccaatgat ctgcgggcat gtaccaagga ctggcattcg 400

gcggcagtaa gaaggcaca aacctgggc aggcctacc ttgtagcagt 450

gataaggagt gtgaagttg gaggtattgc cacagtcccc accaaggatc 500

atcggcctgc atggtgtg gcgagaaaaa gaagcgtgc caccgagatg 550

gcatgtgctg cccagtagc cgctgcaata atggcatctg tatccagtt 600

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gtccaccctt ttaaaaatta ttatttgaag taatttattt acaggaaatg 3000

ttaatgagat gtattttcct atagagatat ttcttacaga aagctttgta 3050

gcagaatata ttgcagcta ttgactttgt aatttaggaa aaatgtataa 3100

taagataaaa tctattaaat tttctcctc taaaaactga aaaaaaaaaa 3150

aaaaaaaaa aaaaaaaaaa 3170

<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys Cys Leu Leu

1 5 10 15

Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser

20 25 30

Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu

35 40 45

Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly

50 55 60

Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala

65 70 75

Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys

80 85 90

His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg

95 100 105

Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr

110 115 120

Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu
 125 130 135
 Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg
 140 145 150
 Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu
 155 160 165
 Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly
 170 175 180
 Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys
 185 190 195
 Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln
 200 205 210
 Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu
 215 220 225
 Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
 230 235 240
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val
 245 250 255
 Cys Gln Lys Ile

<210> 71

<211> 1809

<212> DNA

<213> Homo sapiens

<400> 71

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tggcctccca aagtgtggg attacaggcg tgagccaccg cgcccggcca 100

acatcacgtt tttaaaaatt gattttctca aattcatggc aaatatttcc 150

cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200

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atattttagt aattcatatg ttttagatta taggttttaa catacttg 300

aaaatacttg atgtgtttta aagccttggg cagaaattct gtattgtga 350

ggattgttc tttatcccc ctttaaagt catccgtcct tggctcagga 400

tttgagagc ttgcaccacc aaaaatggca aacatcacca gctcccagat 450

tttgaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500

gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550

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agcaccagag ccaggcagtc actgttctc ctcttggtt ggagtcctt 700

ccttcccagg caaaacttg agaatcaaca cctggagaca gtccctccac 750

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tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850

atacccccag ctttaagat cccagcttct gcagtggaaa tgcctgggtc 900

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gaggcacaag aatcgcttga gccagcttgg gctacaaagt gagactccgt 1800

ctgaaaaga 1809

<210> 72

<211> 363

<212> PRT

<213> Homo sapiens

<400> 72

Met Cys Phe Lys Ala Leu Gly Arg Asn Ser Val Leu Leu Arg Ile

1 5 10 15

Cys Ser Phe Ile Pro Leu Leu Lys Ser Ser Val Leu Gly Ser Gly

20 25 30

Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser

35 40 45

Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr

50 55 60

Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr

65 70 75

Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val
80 85 90

Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val
95 100 105

Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val
110 115 120

Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys
125 130 135

Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys
140 145 150

Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser
155 160 165

Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
170 175 180

Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro
185 190 195

Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu
200 205 210

Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
215 220 225

Ser Ser Glu Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys
230 235 240

Ser Leu Ser Glu Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala
245 250 255

Val Gln Asn Ser Thr Tyr Thr Thr Ser Val Ile Thr Ser Cys Ser
260 265 270

Leu Thr Ser Ser Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser
275 280 285

Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln

290	295	300
Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn		
305	310	315
Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr		
320	325	330
Ser Ser Lys Leu Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg		
335	340	345
Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp		
350	355	360
Leu Ile Arg		

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 73
 aattcatggc aaatatttcc ctcccc 26

<210> 74
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 74
 tggtaaactg gcccaaactc gg 22

<210> 75
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 75

ttaaagtcac cgcctctgg ctcaggattt ggagagcttg caccacaaa 50

<210> 76

<211> 1989

<212> DNA

<213> Homo sapiens

<400> 76

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ccgaatcctg ctttgaaac ttgtcttct gcagagctct gctgttctcc 100

tgcactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150

caccatcact actgccacct ctacgagagc ctggccgtcc gcctggaggt 200

caccgacggc cccccggcca cccccgcta ctgggacggc gagaaggagg 250

tgctggcggg ggcgcgcggc gcacccgcgc ttctgacctg cgtgaaccgc 300

gggcacgtgt ggaccgaccg gcacgtggag gaggtcaac aggtggtgca 350

ctgggaccgg cagccgcccg gggccccga cgaccgcgcg gaccgcctgc 400

tggacctcta cgcgtcgggc gagcgccgcg cctacgggcc ctttttctg 450

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actgcgtatc gagccgctgg aggtcgccga cgagggcacc tactctgcc 550

acctgcacca ccattactgt ggctgcacg aacgccgcgt cttccacctg 600

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cggctccagc cacagcggcg cccagggccc agacccaca ctggcgcgcg 700

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caataaagtc cccattctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77

<211> 341

<212> PRT

<213> Homo sapiens

<400> 77

Met Ala Leu Pro Ser Arg Ile Leu Leu Trp Lys Leu Val Leu Leu
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Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp
20 25 30

Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu
35 40 45

Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro
50 55 60

Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val
65 70 75

Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His
80 85 90

Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His
95 100 105

Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg
110 115 120

Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro
125 130 135

Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu
140 145 150

Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp
155 160 165

Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu
170 175 180

His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala
185 190 195

Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser
200 205 210

Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val
215 220 225

Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln
230 235 240

Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu
245 250 255

Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu
260 265 270

Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn
275 280 285

Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg
290 295 300

Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu
305 310 315

Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp
320 325 330

Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys
335 340

<210> 78

<211> 2243

<212> DNA

<213> Homo sapiens

<400> 78

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<210> 79
<211> 475
<212> PRT
<213> Homo sapiens

<400> 79
Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser
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Thr Tyr Gly Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala
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Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg
35 40 45

Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu
50 55 60

Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys
65 70 75

Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr
80 85 90

Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser
95 100 105

Tyr Leu Ala Val Ala Ser Thr Val Pro Ser Met Leu Cys Leu Val
110 115 120

Ala Asn Phe Leu Leu Val Asn Arg Val Ala Val His Ile Arg Val
125 130 135

Leu Ala Ser Leu Thr Val Ile Leu Ala Ile Phe Met Val Ile Thr
140 145 150

Ala Leu Val Lys Val Asp Thr Ser Ser Trp Thr Arg Gly Phe Phe
155 160 165

Ala Val Thr Ile Val Cys Met Val Ile Leu Ser Gly Ala Ser Thr
170 175 180

Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser Phe Pro Met

185	190	195
Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly Gly Thr		
200	205	210
Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser Asp		
215	220	225
Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe		
230	235	240
Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu		
245	250	255
Tyr Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe		
260	265	270
Ser Gly Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser		
275	280	285
Val Ala Ser Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro		
290	295	300
Ile Leu Lys Lys Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val		
305	310	315
Phe Phe Ile Thr Ser Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile		
320	325	330
Glu Ser Leu Asn Lys Gly Ser Gly Ser Leu Trp Thr Thr Lys Phe		
335	340	345
Phe Ile Pro Leu Thr Thr Phe Leu Leu Tyr Asn Phe Ala Asp Leu		
350	355	360
Cys Gly Arg Gln Leu Thr Ala Trp Ile Gln Val Pro Gly Pro Asn		
365	370	375
Ser Lys Ala Leu Pro Gly Phe Val Leu Leu Arg Thr Cys Leu Ile		
380	385	390
Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro Arg Val His Leu Lys		
395	400	405

Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser
410 415 420

Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu
425 430 435

Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly
440 445 450

Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser
455 460 465

Ala Cys Ser Thr Leu Leu Val His Leu Ile
470 475

<210> 80

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 80

ttttgcggtc accattgtct gc 22

<210> 81

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 81

cgtaggtgac acagaagccc agg 23

<210> 82

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 82

tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83

<211> 1844

<212> DNA

<213> Homo sapiens

<400> 83

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aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200

ctatgagcag ctgtcaagg tggtagctg ggggctcaat cggaccctga 250

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aaaacacgac ccacacgagg acctcgcat aaagtattt cggaaaaaa 1800
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<211> 567

<212> PRT

<213> Homo sapiens

<400> 84

Met Ala Pro Leu Ala Leu His Leu Leu Val Leu Val Pro Ile Leu
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Leu Ser Leu Val Ala Ser Gln Asp Trp Lys Ala Glu Arg Ser Gln
20 25 30

Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu
35 40 45

Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln
50 55 60

Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala
65 70 75

Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala
80 85 90

Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn
95 100 105

Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser
110 115 120

His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu
125 130 135

Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His
140 145 150

Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys
155 160 165

Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu
170 175 180

Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys
185 190 195

Ala Leu Gly Cys Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr
200 205 210

Leu Leu Glu Tyr Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala
215 220 225

Val Gln Leu Leu Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr
230 235 240

Leu Ser Phe Ala Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp
245 250 255

Arg Leu Gln Tyr Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro
260 265 270

Arg Ala Leu Leu Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala
275 280 285

Pro Val Val Ala Met Thr Gln Gly Pro His Asp Val His Val Gln
290 295 300

Ile Glu Thr Ser Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala
305 310 315

Asp Val Val Leu Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile
320 325 330

Thr Phe Ser Pro Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg
335 340 345

Arg Leu His Tyr Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg
350 355 360

Arg Pro Phe Trp Arg Glu Glu His Ile Glu Gly Gly His Ser Asn
365 370 375

Thr Asp Arg Pro Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu
380 385 390

Gly Ala Leu Leu Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala
395 400 405

Ala Phe Ala Gly Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu

410	415	420
Asp Asp Val Ala Ala Leu His Gly Pro Val Val Arg Gln Leu Trp		
425	430	435
Asp Gly Thr Gly Val Val Lys Arg Trp Ala Glu Asp Gln His Ser		
440	445	450
Gln Gly Gly Phe Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu		
455	460	465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly		
470	475	480
Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys		
485	490	495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro		
500	505	510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu		
515	520	525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp		
530	535	540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu		
545	550	555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His		
560	565	

<210> 85

<211> 3316

<212> DNA

<213> Homo sapiens

<400> 85

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tattacagat aaaaaa 3316

<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

Met Asp Ala Leu Lys Pro Pro Cys Leu Trp Arg Asn His Glu Arg
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Gly Lys Lys Asp Arg Asp Ser Cys Gly Arg Lys Asn Ser Glu Pro
20 25 30

Gly Ser Pro His Ser Leu Glu Ala Leu Arg Asp Ala Ala Pro Ser
35 40 45

Gln Gly Leu Asn Phe Leu Leu Leu Phe Thr Lys Met Leu Phe Ile
50 55 60

Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala Leu Ile Cys
65 70 75

Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile Thr Arg
80 85 90

Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser Val
95 100 105

Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn
110 115 120

Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu
125 130 135

Val Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu
140 145 150

Gly Tyr Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys
155 160 165

Gln Val Ser Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His
170 175 180

Lys Gly Tyr Lys Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala
185 190 195

Gln Asn Arg Pro Glu Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr

200	205	210
Tyr Ser Met Val Ala Val Pro Leu Tyr Asp Thr Leu Gly Pro Glu		
215	220	225
Ala Ile Val His Ile Val Asn Lys Ala Asp Ile Ala Met Val Ile		
230	235	240
Cys Asp Thr Pro Gln Lys Ala Leu Val Leu Ile Gly Asn Val Glu		
245	250	255
Lys Gly Phe Thr Pro Ser Leu Lys Val Ile Ile Leu Met Asp Pro		
260	265	270
Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu Lys Ser Gly Ile Glu		
275	280	285
Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Gly Lys Glu His Phe		
290	295	300
Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser Val Ile Cys		
305	310	315
Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met Ile Thr		
320	325	330
His Gln Asn Ile Val Ser Asn Ala Ala Ala Phe Leu Lys Cys Val		
335	340	345
Glu His Ala Tyr Glu Pro Thr Pro Asp Asp Val Ala Ile Ser Tyr		
350	355	360
Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val		
365	370	375
Tyr Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg		
380	385	390
Leu Leu Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro		
395	400	405
Ala Val Pro Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn		
410	415	420

Glu Ala Lys Thr Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val
425 430 435

Ser Ser Lys Phe Lys Glu Leu Gln Lys Gly Ile Ile Arg His Asp
440 445 450

Ser Phe Trp Asp Lys Leu Ile Phe Ala Lys Ile Gln Asp Ser Leu
455 460 465

Gly Gly Arg Val Arg Val Ile Val Thr Gly Ala Ala Pro Met Ser
470 475 480

Thr Ser Val Met Thr Phe Phe Arg Ala Ala Met Gly Cys Gln Val
485 490 495

Tyr Glu Ala Tyr Gly Gln Thr Glu Cys Thr Gly Gly Cys Thr Phe
500 505 510

Thr Leu Pro Gly Asp Trp Thr Ser Gly His Val Gly Val Pro Leu
515 520 525

Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala Asp Met Asn Tyr
530 535 540

Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys Gly Thr Asn
545 550 555

Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln Glu Ala
560 565 570

Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg Trp
575 580 585

Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile
590 595 600

Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu
605 610 615

Asn Ile Tyr Asn Arg Ser Gln Pro Val Leu Gln Ile Phe Val His
620 625 630

Gly Glu Ser Leu Arg Ser Ser Leu Val Gly Val Val Val Pro Asp

635	640	645
Thr Asp Val Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly		
650	655	660
Ser Phe Glu Glu Leu Cys Gln Asn Gln Val Val Arg Glu Ala Ile		
665	670	675
Leu Glu Asp Leu Gln Lys Ile Gly Lys Glu Ser Gly Leu Lys Thr		
680	685	690
Phe Glu Gln Val Lys Ala Ile Phe Leu His Pro Glu Pro Phe Ser		
695	700	705
Ile Glu Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Gly		
710	715	720
Glu Leu Ser Lys Tyr Phe Arg Thr Gln Ile Asp Ser Leu Tyr Glu		
725	730	735
His Ile Gln Asp		

<210> 87

<211> 2725

<212> DNA

<213> Homo sapiens

<400> 87

ggaggcggag gccgcggcga gccgggccga gcagtgagg ccctagcggg 50

gcccgagcgg ggcccggggc ccctaagcca ttctgaagt catgggctgg 100

ccaggacatt ggtgaccgc caatccgta tggacgactg gaagcccagc 150

ccctcatca agccctttgg ggctcggaag aagcggagct ggtaccttac 200

ctggaagtat aaactgacaa accagcgggc cctgcggaga ttctgcaga 250

caggggccgt gcttttctg ctggtgactg tcattgtcaa tatcaagttg 300

atcctggaca ctcggcgagc catcagtga gccaatgaag acccagagcc 350

agagcaagac tatgatgagg ccctaggccg cctggagccc ccacggcgca 400
gaggcagtgg tccccggcgg gtcctggacg tagaggtgta ttcaagtcgc 450
agcaaagtat atgtggcagt ggatggcacc acggtgctgg aggatgaggc 500
ccgggagcag ggccggggca tccatgtcat tgtcctcaac caggccacgg 550
gccacgtgat ggcaaacgt gtgttgaca cgtactcacc tcatgaggat 600
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agacagatgt gccattgagc tcagcagaag aggcagagtg cactgggca 900
gacacagagc tgaaccgtc ccgccggcgc ttctgcagca aagttgaggg 950
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caaagctgga taagttggtc attgattaaa aaaggagaag ccctctggga 2700

aaaaaaaaa aaaaaaaaaa aaaaa 2725

<210> 88

<211> 660

<212> PRT

<213> Homo sapiens

<400> 88

Met Asp Asp Trp Lys Pro Ser Pro Leu Ile Lys Pro Phe Gly Ala

1 5 10 15

Arg Lys Lys Arg Ser Trp Tyr Leu Thr Trp Lys Tyr Lys Leu Thr

20 25 30

Asn Gln Arg Ala Leu Arg Arg Phe Cys Gln Thr Gly Ala Val Leu

35 40 45

Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp

50 55 60

Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu

65 70 75

Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg

80 85 90

Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser

95 100 105

Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu

110 115 120

Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val

125 130 135

Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp

140 145 150

Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn
155 160 165

Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu
170 175 180

Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser
185 190 195

Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp
200 205 210

Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His
215 220 225

Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu
230 235 240

Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His
245 250 255

Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser
260 265 270

Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr
275 280 285

Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu
290 295 300

Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu
305 310 315

Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro
320 325 330

Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met
335 340 345

Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro
350 355 360

Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser

365	370	375
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val		
380	385	390
Val Leu Glu Glu Asp Leu Asp Ile Ala Val Asp Phe Phe Ser Phe		
395	400	405
Leu Ser Gln Ser Ile His Leu Leu Glu Glu Asp Asp Ser Leu Tyr		
410	415	420
Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr Glu His Thr Ala Glu		
425	430	435
Asp Pro Ala Leu Leu Tyr Arg Val Glu Thr Met Pro Gly Leu Gly		
440	445	450
Trp Val Leu Arg Arg Ser Leu Tyr Lys Glu Glu Leu Glu Pro Lys		
455	460	465
Trp Pro Thr Pro Glu Lys Leu Trp Asp Trp Asp Met Trp Met Arg		
470	475	480
Met Pro Glu Gln Arg Arg Gly Arg Glu Cys Ile Ile Pro Asp Val		
485	490	495
Ser Arg Ser Tyr His Phe Gly Ile Val Gly Leu Asn Met Asn Gly		
500	505	510
Tyr Phe His Glu Ala Tyr Phe Lys Lys His Lys Phe Asn Thr Val		
515	520	525
Pro Gly Val Gln Leu Arg Asn Val Asp Ser Leu Lys Lys Glu Ala		
530	535	540
Tyr Glu Val Glu Val His Arg Leu Leu Ser Glu Ala Glu Val Leu		
545	550	555
Asp His Ser Lys Asn Pro Cys Glu Asp Ser Phe Leu Pro Asp Thr		
560	565	570
Glu Gly His Thr Tyr Val Ala Phe Ile Arg Met Glu Lys Asp Asp		
575	580	585

Asp Phe Thr Thr Trp Thr Gln Leu Ala Lys Cys Leu His Ile Trp
590 595 600

Asp Leu Asp Val Arg Gly Asn His Arg Gly Leu Trp Arg Leu Phe
605 610 615

Arg Lys Lys Asn His Phe Leu Val Val Gly Val Pro Ala Ser Pro
620 625 630

Tyr Ser Val Lys Lys Pro Pro Ser Val Thr Pro Ile Phe Leu Glu
635 640 645

Pro Pro Pro Lys Glu Glu Gly Ala Pro Gly Ala Pro Glu Gln Thr
650 655 660

<210> 89

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 89

gatggcaaaa cgtgtgtttg acacg 25

<210> 90

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 90

cctcaaccag gccacgggcc ac 22

<210> 91

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 91

cccaggcaga gatgcagtac aggc 24

<210> 92

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 92

cctccagtag gtggatggat tggctc 26

<210> 93

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 93

ctcacctcat gaggatgagg ccatggtgct attcctcaac atggtag 47

<210> 94

<211> 3037

<212> DNA

<213> Homo sapiens

<400> 94

cggacgcgtg ggctgctggt ggaaggcct aaagaactgg aaagcccact 50

ctcttgaac caccacacct gtttaaagaa cctaagcacc atttaaagcc 100

actggaaatt tgtgtctag tggttgtggg tgaataaagg agggcagaat 150

ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtgggat 200

gttacgtggc cggaatcatt cccttggtg ttaatttctc agaggaacga 250

ctgaagctgg tgactgtttt ggggtgctggc ctctctgtg gaactgtct 300
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tcatgttct ggtggaccag attggttaact cccatgtgca ttctactgac 550
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ctagtccttc aaaactatat ggtgcctag attctctctg gaaactgact 3000

ttgtcaaata aatagcagat ttagtgtca aaaaaaa 3037

<210> 95

<211> 307

<212> PRT

<213> Homo sapiens

<400> 95

Met Asp Asp Phe Ile Ser Ile Ser Leu Leu Ser Leu Ala Met Leu

1 5 10 15

Val Gly Cys Tyr Val Ala Gly Ile Ile Pro Leu Ala Val Asn Phe

20 25 30

Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu

35 40 45

Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His

50 55 60

Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser

65	70	75
Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser		
80	85	90
Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His		
95	100	105
Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu		
110	115	120
Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp		
125	130	135
Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu		
140	145	150
Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala		
155	160	165
Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val		
170	175	180
Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser		
185	190	195
Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His		
200	205	210
Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr		
215	220	225
Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val		
230	235	240
Asn Ala Thr Gly Val Ala Met Leu Phe Ser Ala Gly Thr Phe Leu		
245	250	255
Tyr Val Ala Thr Val His Val Leu Pro Glu Val Gly Gly Ile Gly		
260	265	270
His Ser His Lys Pro Asp Ala Thr Gly Gly Arg Gly Leu Ser Arg		
275	280	285

Leu Glu Val Ala Ala Leu Val Leu Gly Cys Leu Ile Pro Leu Ile
290 295 300

Leu Ser Val Gly His Gln His
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<210> 96

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 96

gttgtgggtg aataaaggag ggcag 25

<210> 97

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 97

ctgtgctcat gtcatggac aactg 25

<210> 98

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 98

ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtgggat 50

<210> 99

<211> 1429

<212> DNA

<213> Homo sapiens

<400> 99

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ctgattttga gatgatgggc ttgggaaacg ggcgtcgag catgaagtcg 150
ccgcccctcg tctggccgc cctggtggcc tgcacatcg tcttgggctt 200
caactactgg attgcgagct cccggagcgt ggacctccag acacggatca 250
tggagctgga aggcagggtc cgcaggcgcg ctgcagagag aggcgccgtg 300
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ggcctgccac acacagaggt gccacaaggg aagggaacg tgcttggtaa 800
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gagcctcaga gggacaggct gccgcaggag ccaggccggg agcaggtggt 950
ggaagacaga cctgtagggt gaagaggctt cgggggagcc ggagaactgg 1000
gccagacccc acaggtgcag gctgccctgt cagtgagcca ggaaaatcca 1050

<210> 100
<211> 401
<212> PRT
<213> Homo sapiens

<400> 100

Met Met Gly Leu Gly Asn Gly Arg Arg Ser Met Lys Ser Pro Pro
1 5 10 15

Leu Val Leu Ala Ala Leu Val Ala Cys Ile Ile Val Leu Gly Phe
20 25 30

Asn Tyr Trp Ile Ala Ser Ser Arg Ser Val Asp Leu Gln Thr Arg
35 40 45

Ile Met Glu Leu Glu Gly Arg Val Arg Arg Ala Ala Ala Glu Arg
50 55 60

Gly Ala Val Glu Leu Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu
65 70 75

Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser Ser His Asn Phe
80 85 90

Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu Lys Ala Val
95 100 105

Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg Val Leu
110 115 120

Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu Gln
125 130 135

Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg
140 145 150

Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu
155 160 165

Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys
170 175 180

Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp
185 190 195

Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu
200 205 210

Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly
215 220 225

Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser
230 235 240

Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr
245 250 255

Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu
260 265 270

Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val
275 280 285

Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro
290 295 300

Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met
305 310 315

Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu

320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu		
335	340	345
Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser		
350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile		
365	370	375
Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu		
380	385	390
Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu		
395	400	

<210> 101
 <211> 3671
 <212> DNA
 <213> Homo sapiens

<400> 101
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 ggagctcacc aaccatagca gctgccaaga gccccaggc cctgggtccc 150
 tgccatgggg gagccaaggg aaacctgggg cctgctggat ggcttcccga 200
 tttcgcggg ttgtgttgt gctgatagat gctctcgat ttgacttcgc 250
 ccagccccag cattcacacg tgcctagaga gcctctgtc tcctaccct 300
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<210> 102

<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

Met Gln Lys Ala Ser Val Leu Leu Phe Leu Ala Trp Val Cys Phe

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Leu Phe Tyr Ala Gly Ile Ala Leu Phe Thr Ser Gly Phe Leu Leu

20 25 30

Thr Arg Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro

35 40 45

Gly Pro Gly Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala

50 55 60

Cys Trp Met Ala Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile

65 70 75

Asp Ala Leu Arg Phe Asp Phe Ala Gln Pro Gln His Ser His Val

80 85 90

Pro Arg Glu Pro Pro Val Ser Leu Pro Phe Leu Gly Lys Leu Ser

95 100 105

Ser Leu Gln Arg Ile Leu Glu Ile Gln Pro His His Ala Arg Leu

110 115 120

Tyr Arg Ser Gln Val Asp Pro Pro Thr Thr Thr Met Gln Arg Leu

125 130 135

Lys Ala Leu Thr Thr Gly Ser Leu Pro Thr Phe Ile Asp Ala Gly

140 145 150

Ser Asn Phe Ala Ser His Ala Ile Val Glu Asp Asn Leu Ile Lys

155 160 165

Gln Leu Thr Ser Ala Gly Arg Arg Val Val Phe Met Gly Asp Asp

170 175 180

Thr Trp Lys Asp Leu Phe Pro Gly Ala Phe Ser Lys Ala Phe Phe

185 190 195

Phe Pro Ser Phe Asn Val Arg Asp Leu Asp Thr Val Asp Asn Gly

200	205	210
Ile Leu Glu His Leu Tyr Pro Thr Met Asp Ser Gly Glu Trp Asp		
215	220	225
Val Leu Ile Ala His Phe Leu Gly Val Asp His Cys Gly His Lys		
230	235	240
His Gly Pro His His Pro Glu Met Ala Lys Lys Leu Ser Gln Met		
245	250	255
Asp Gln Val Ile Gln Gly Leu Val Glu Arg Leu Glu Asn Asp Thr		
260	265	270
Leu Leu Val Val Ala Gly Asp His Gly Met Thr Thr Asn Gly Asp		
275	280	285
His Gly Gly Asp Ser Glu Leu Glu Val Ser Ala Ala Leu Phe Leu		
290	295	300
Tyr Ser Pro Thr Ala Val Phe Pro Ser Thr Pro Pro Glu Glu Pro		
305	310	315
Glu Val Ile Pro Gln Val Ser Leu Val Pro Thr Leu Ala Leu Leu		
320	325	330
Leu Gly Leu Pro Ile Pro Phe Gly Asn Ile Gly Glu Val Met Ala		
335	340	345
Glu Leu Phe Ser Gly Gly Glu Asp Ser Gln Pro His Ser Ser Ala		
350	355	360
Leu Ala Gln Ala Ser Ala Leu His Leu Asn Ala Gln Gln Val Ser		
365	370	375
Arg Phe Leu His Thr Tyr Ser Ala Ala Thr Gln Asp Leu Gln Ala		
380	385	390
Lys Glu Leu His Gln Leu Gln Asn Leu Phe Ser Lys Ala Ser Ala		
395	400	405
Asp Tyr Gln Trp Leu Leu Gln Ser Pro Lys Gly Ala Glu Ala Thr		
410	415	420

Leu Pro Thr Val Ile Ala Glu Leu Gln Gln Phe Leu Arg Gly Ala
425 430 435

Arg Ala Met Cys Ile Glu Ser Trp Ala Arg Phe Ser Leu Val Arg
440 445 450

Met Ala Gly Gly Thr Ala Leu Leu Ala Ala Ser Cys Phe Ile Cys
455 460 465

Leu Leu Ala Ser Gln Trp Ala Ile Ser Pro Gly Phe Pro Phe Cys
470 475 480

Pro Leu Leu Leu Thr Pro Val Ala Trp Gly Leu Val Gly Ala Ile
485 490 495

Ala Tyr Ala Gly Leu Leu Gly Thr Ile Glu Leu Lys Leu Asp Leu
500 505 510

Val Leu Leu Gly Ala Val Ala Ala Val Ser Ser Phe Leu Pro Phe
515 520 525

Leu Trp Lys Ala Trp Ala Gly Trp Gly Ser Lys Arg Pro Leu Ala
530 535 540

Thr Leu Phe Pro Ile Pro Gly Pro Val Leu Leu Leu Leu Phe
545 550 555

Arg Leu Ala Val Phe Phe Ser Asp Ser Phe Val Val Ala Glu Ala
560 565 570

Arg Ala Thr Pro Phe Leu Leu Gly Ser Phe Ile Leu Leu Leu Val
575 580 585

Val Gln Leu His Trp Glu Gly Gln Leu Leu Pro Pro Lys Leu Leu
590 595 600

Thr Met Pro Arg Leu Gly Thr Ser Ala Thr Thr Asn Pro Pro Arg
605 610 615

His Asn Gly Ala Tyr Ala Leu Arg Leu Gly Ile Gly Leu Leu Leu
620 625 630

Cys Thr Arg Leu Ala Gly Leu Phe His Arg Cys Pro Glu Glu Thr

635	640	645
Pro Val Cys His Ser Ser Pro Trp Leu Ser Pro Leu Ala Ser Met		
650	655	660
Val Gly Gly Arg Ala Lys Asn Leu Trp Tyr Gly Ala Cys Val Ala		
665	670	675
Ala Leu Val Ala Leu Leu Ala Ala Val Arg Leu Trp Leu Arg Arg		
680	685	690
Tyr Gly Asn Leu Lys Ser Pro Glu Pro Pro Met Leu Phe Val Arg		
695	700	705
Trp Gly Leu Pro Leu Met Ala Leu Gly Thr Ala Ala Tyr Trp Ala		
710	715	720
Leu Ala Ser Gly Ala Asp Glu Ala Pro Pro Arg Leu Arg Val Leu		
725	730	735
Val Ser Gly Ala Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu		
740	745	750
Ala Ala Ser Gly Leu Ala Leu Leu Leu Trp Lys Pro Val Thr Val		
755	760	765
Leu Val Lys Ala Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu		
770	775	780
Thr Pro Phe Ser Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr		
785	790	795
Val Val Pro Gln Ile Tyr Arg His Met Gln Glu Glu Phe Arg Gly		
800	805	810
Arg Leu Glu Arg Thr Lys Ser Gln Gly Pro Leu Thr Val Ala Ala		
815	820	825
Tyr Gln Leu Gly Ser Val Tyr Ser Ala Ala Met Val Thr Ala Leu		
830	835	840
Thr Leu Leu Ala Phe Pro Leu Leu Leu Leu His Ala Glu Arg Ile		
845	850	855

Ser Leu Val Phe Leu Leu Leu Phe Leu Gln Ser Phe Leu Leu Leu
860 865 870

His Leu Leu Ala Ala Gly Ile Pro Val Thr Thr Pro Gly Pro Phe
875 880 885

Thr Val Pro Trp Gln Ala Val Ser Ala Trp Ala Leu Met Ala Thr
890 895 900

Gln Thr Phe Tyr Ser Thr Gly His Gln Pro Val Phe Pro Ala Ile
905 910 915

His Trp His Ala Ala Phe Val Gly Phe Pro Glu Gly His Gly Ser
920 925 930

Cys Thr Trp Leu Pro Ala Leu Leu Val Gly Ala Asn Thr Phe Ala
935 940 945

Ser His Leu Leu Phe Ala Val Gly Cys Pro Leu Leu Leu Leu Trp
950 955 960

Pro Phe Leu Cys Glu Ser Gln Gly Leu Arg Lys Arg Gln Gln Pro
965 970 975

Pro Gly Asn Glu Ala Asp Ala Arg Val Arg Pro Glu Glu Glu Glu
980 985 990

Glu Pro Leu Met Glu Met Arg Leu Arg Asp Ala Pro Gln His Phe
995 1000 1005

Tyr Ala Ala Leu Leu Gln Leu Gly Leu Lys Tyr Leu Phe Ile Leu
1010 1015 1020

Gly Ile Gln Ile Leu Ala Cys Ala Leu Ala Ala Ser Ile Leu Arg
1025 1030 1035

Arg His Leu Met Val Trp Lys Val Phe Ala Pro Lys Phe Ile Phe
1040 1045 1050

Glu Ala Val Gly Phe Ile Val Ser Ser Val Gly Leu Leu Leu Gly
1055 1060 1065

Ile Ala Leu Val Met Arg Val Asp Gly Ala Val Ser Ser Trp Phe

1070

1075

1080

Arg Gln Leu Phe Leu Ala Gln Gln Arg
1085

<210> 103

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 103

tgccgctgcc gccgctgtcg ctgttgctcc tggcggcgcc ttggggacgg 50

gcagttccct gtgtctctgg tggtttcct aaacctgcaa acatcacctt 100

cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc 150

ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200

cccaccagag gtggcactga ctacagatga gaagtcatt tctgtgtcc 250

tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300

atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350

taaatcaaac agaacgtggt ccagtggtg gaccaaccac acgctgggtc 400

tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450

gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500

gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550

atgttttgcc catatctatt accgtgttc tttttctgt gatgggctat 600

tccatctacc gatatacca cgttggcaaa gagaaacacc cagcaaattt 650

gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700

aaaaaatcgt gattaacttt atcacctca atatctcgga tgattctaaa 750

atttctcatc aggatatgag ttactggga aaaagcagtg atgtatccag 800

ccttaatgat cctcagccca gcgggaacct gagggcccct caggaggaag 850
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aatttttgt 900
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<210> 104

<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

Met Ser Tyr Asn Gly Leu His Gln Arg Val Phe Lys Glu Leu Lys
1 5 10 15

Leu Leu Thr Leu Cys Ser Ile Ser Ser Gln Ile Gly Pro Pro Glu
20 25 30

Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr
35 40 45

Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser
50 55 60

Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu
65 70 75

Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His
80 85 90

Thr Leu Val Leu Thr Trp Leu Glu Pro Asn Thr Leu Tyr Cys Val
95 100 105

His Val Glu Ser Phe Val Pro Gly Pro Pro Arg Arg Ala Gln Pro
110 115 120

Ser Glu Lys Gln Cys Ala Arg Thr Leu Lys Asp Gln Ser Ser Glu
125 130 135

Phe Lys Ala Lys Ile Ile Phe Trp Tyr Val Leu Pro Ile Ser Ile
140 145 150

Thr Val Phe Leu Phe Ser Val Met Gly Tyr Ser Ile Tyr Arg Tyr
155 160 165

Ile His Val Gly Lys Glu Lys His Pro Ala Asn Leu Ile Leu Ile
170 175 180

Tyr Gly Asn Glu Phe Asp Lys Arg Phe Phe Val Pro Ala Glu Lys
185 190 195

Ile Val Ile Asn Phe Ile Thr Leu Asn Ile Ser Asp Asp Ser Lys
200 205 210

Ile Ser His Gln Asp Met Ser Leu Leu Gly Lys Ser Ser Asp Val
215 220 225

Ser Ser Leu Asn Asp Pro Gln Pro Ser Gly Asn Leu Arg Pro Pro
230 235 240

Gln Glu Glu Glu Glu Val Lys His Leu Gly Tyr Ala Ser His Leu
245 250 255

Met Glu Ile Phe Cys Asp Ser Glu Glu Asn Thr Glu Gly Thr Ser
260 265 270

Leu Thr Gln Gln Glu Ser Leu Ser Arg Thr Ile Pro Pro Asp Lys
275 280 285

Thr Val Ile Glu Tyr Glu Tyr Asp Val Arg Thr Thr Asp Ile Cys
290 295 300

Ala Gly Pro Glu Glu Gln Glu Leu Ser Leu Gln Glu Glu Val Ser
305 310 315

Thr Gln Gly Thr Leu Leu Glu Ser Gln Ala Ala Leu Ala Val Leu
320 325 330

Gly Pro Gln Thr Leu Gln Tyr Ser Tyr Thr Pro Gln Leu Gln Asp
335 340 345

Leu Asp Pro Leu Ala Gln Glu His Thr Asp Ser Glu Glu Gly Pro
350 355 360

Glu Glu Glu Pro Ser Thr Thr Leu Val Asp Trp Asp Pro Gln Thr
365 370 375

Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser
380 385 390

Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly
395 400 405

Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro
410 415 420

Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly

425 430 435

Leu Tyr Val Gln Met Glu Asn
440

<210> 105

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 105

cgctgctgct gttgctcctg g 21

<210> 106

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 106

cagtgtgccca ggactttg 18

<210> 107

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 107

agtcgcaggc agcgttgg 18

<210> 108

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 108

ctcctccgag tctgtgtgct cctgc 25

<210> 109

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 109

ggacgggcag ttcctgtgt ctctgggtgt ttgcctaaac ctgcaaaca 50

c 51

<210> 110

<211> 1114

<212> DNA

<213> Homo sapiens

<400> 110

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cggcagcctg cgtctgcat ggggctcggg ttgaggggt ggggacgtcc 100

tctgtgact gtggccaccg ccctgatgct gccctgaag cccccgcag 150

gctcctgggg ggcccagatc atcgggggcc acgaggtgac cccccactcc 200

aggccctaca tggcatccgt gcgttcggg ggccaacatc actgcggagg 250

cttctgctg cgagcccgt ggggtgtctc ggccgccac tgcttcagcc 300

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 gccgtccag gcctggaatg ttccgtggct gggcccccacg ggaagcctga 1000
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 aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val

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Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp

20 25 30

Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg

35 40 45

Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly
50 55 60

Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys
65 70 75

Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala
80 85 90

His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile
95 100 105

Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala
110 115 120

Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly
125 130 135

Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro
140 145 150

Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val
155 160 165

Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val
170 175 180

Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His
185 190 195

Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg
200 205 210

Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg
215 220 225

Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly
230 235 240

Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val
245 250 255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly

260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
275 280

<210> 112

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gacgtctgca acagctcctg gaag 24

<210> 113

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 113

cgagaaggaa acgaggccgt gag 23

<210> 114

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 114

tgacacttac catgctctgc accgcagtg gggacagcca caga 44

<210> 115

<211> 1808

<212> DNA

<213> Homo sapiens

<400> 115

gagctacca ggcggctggt gtgcagcaag ctccgcgccg actccggacg 50
cctgacgct gacgcctgtc cccggcccgg catgagccgc tacctgtctc 100
cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150
tatgtaccg gtggggcttg cccagcaag gccaccatcc ctgggaagac 200
ggatcatctg acgggcgcca acacaggcat cgggaagcag accgccttgg 250
aactggccag gagaggagc aacatcatcc tggcctgccg agacatggag 300
aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatacca 350
tgtcaacgc cggcacctgg acttggttc cctcaagtct atccgagagt 400
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 tgggaacccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750
 caccttccta tcaattctca tggtagtcca aactgcagac tctcaaactt 1800
 gctcattt 1808

<210> 116

<211> 331

<212> PRT

<213> Homo sapiens

<400> 116

Met	Ser	Arg	Tyr	Leu	Leu	Pro	Leu	Ser	Ala	Leu	Gly	Thr	Val	Ala
1		5		10				15						

Gly	Ala	Ala	Val	Leu	Leu	Lys	Asp	Tyr	Val	Thr	Gly	Gly	Ala	Cys
		20			25					30				

Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
35 40 45

Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
50 55 60

Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
65 70 75

Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
80 85 90

Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
95 100 105

Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
110 115 120

Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
125 130 135

Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
140 145 150

Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
155 160 165

Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
170 175 180

His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
185 190 195

Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
200 205 210

Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
215 220 225

Asn Ala Leu His Pro Gly Val Ala Arg Thr Glu Leu Gly Arg His
230 235 240

Thr Gly Ile His Gly Ser Thr Phe Ser Ser Thr Thr Leu Gly Pro

245	250	255
Ile Phe Trp Leu Leu Val Lys Ser Pro Glu Leu Ala Ala Gln Pro		
260	265	270
Ser Thr Tyr Leu Ala Val Ala Glu Glu Leu Ala Asp Val Ser Gly		
275	280	285
Lys Tyr Phe Asp Gly Leu Lys Gln Lys Ala Pro Ala Pro Glu Ala		
290	295	300
Glu Asp Glu Glu Val Ala Arg Arg Leu Trp Ala Glu Ser Ala Arg		
305	310	315
Leu Val Gly Leu Glu Ala Pro Ser Val Arg Glu Gln Pro Leu Pro		
320	325	330

Arg

<210> 117

<211> 2249

<212> DNA

<213> Homo sapiens

<400> 117

gaagttcgcg agcgctggca tgtggtcctg gggcgcggtt ggcggcgctg 50

ctggcgggtgc tggcgctcgg gacaggagac ccagaaaggg ctgcggctcg 100

gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccg 150

agcgccggct gctggggctg ctgaggcggg acctgcgcgg ggaggaggcg 200

cggctgcggg acctgactag attctacgac aaggtacttt ctttgcata 250

ggattcaaca acccctgtgg ctaaccctct gcttgcattt actctcatca 300

aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350

gagaacatcc gagctctgaa ggatggctat gagaaggtgg agcaagacct 400

tccagccttt gaggaccttg agggagcagc aagggccttg atcgggctgc 450

aggacgtgta catgctcaat gtgaaaggcc tggcccaggagg tgtctttcag 500
agagtcactg gctctgccat cactgacctg tacagcccca aacggctctt 550
ttctctcaca ggggatgact gcttccaagt tggcaagggtg gcctatgaca 600
tgggggatta ttaccatgcc attccatggc tggaggaggc tgcagtctc 650
ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700
agatgccttg gatcacttgg ccttggctta ttccgggca ggaaatgtt 750
cgtgtgcct cagcctctct cgggagttc ttctctacag cccagataat 800
aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850
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acctgcagac cagagacacc tacgaggggc tatgtcagac cctgggttcc 950
cagcccactc tctaccagat ccctagcctc tactgttct atgagaccaa 1000
ttccaacgcc tacctgtgc tccagcccat ccggaaggag gtcacccacc 1050
tggagcccta cattgtctc taccatgact tcgtcagtga ctcagaggct 1100
cagaaaatta gagaactgc agaaccatgg ctacagaggt cagtgggtgc 1150
atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtgcct 1200
ggctgaagga cactgttgac caaaaactgg tgacctcaa ccaccgatt 1250
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gcaacattta tgatctatct gagtcgggtg gaagctggag gagccacagc 1450
cttcatctat gccaacctca gcgtgcctgt ggtaggaat gcagcactgt 1500
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gctggctgtc ctgtcctggt gggagataag tgggtggcca acaagtggat 1600
 acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650
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 cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggc 2050
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 agcccaagca gggagtgtcc cctcccaga agcatatccc agatgagtgg 2150
 tacattatat aaggattttt ttaagtga aaacaacttt cttttcttt 2200
 tgtatgatgg tttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met	Gly	Pro	Gly	Ala	Arg	Leu	Ala	Ala	Leu	Ala	Val	Leu	Ala
1		5		10		15							

Leu	Gly	Thr	Gly	Asp	Pro	Glu	Arg	Ala	Ala	Ala	Arg	Gly	Asp	Thr
		20		25		30								

Phe	Ser	Ala	Leu	Thr	Ser	Val	Ala	Arg	Ala	Leu	Ala	Pro	Glu	Arg
		35		40		45								

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
110 115 120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
185 190 195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
200 205 210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
215 220 225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
230 235 240

Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu
245 250 255

Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr

260	265	270
Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala		
275	280	285
Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr		
290	295	300
Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr		
305	310	315
Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala		
320	325	330
Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu		
335	340	345
Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala		
350	355	360
Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val		
365	370	375
Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser		
380	385	390
Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr		
395	400	405
Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro		
410	415	420
Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly		
425	430	435
His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro		
440	445	450
Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile		
455	460	465
Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr		
470	475	480

Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp
485 490 495

Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His
500 505 510

Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys
515 520 525

Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser
530 535 540

Ser Pro Glu Asp

<210> 119

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 119

cgggacagga gaccagaaa ggg 23

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

ggccaagtga tccaaggcat cttc 24

<210> 121

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattgggg 49

<210> 122

<211> 1778

<212> DNA

<213> Homo sapiens

<400> 122

gagataggga gtctggggtt aagttcctgc tccatctcag gagcccctgc 50

tcccaccct aggaagccac cagactccac ggtgtggggc caatcaggtg 100

gaatcgggcc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150

ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgccg 200

cgcggggact cggagcaggt gcgctactgc gcgcgttct cctacctctg 250

gctcaagttt tcactatca tctattccac cgtgttctgg ctgattgggg 300

ccctggctct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350

aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcactctct 400

gggcgtcgtc atgttcatgg tctccttcat tgggtgtctg gcgtccctcc 450

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ctcatcatgg agctcattgg tggcgtggtg gccttgacct tccggaacca 550

gaccattgac ttctgaacg acaacattcg aagaggaatt gagaactact 600

atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650

aagtgtgtg gcggggagga ctaccgagat tggagcaaga atcagtacca 700

cgactgcagt gcccctggac ccctggcctg tggggtgccc tacacctgct 750

gcatcaggaa cagcacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800

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gtacagataa caggagtctc tgactaatca aagctggtat ttccccgc 1700
gtctattct tgccctccc ccaaccagt ttgtaataa acaataaaaa 1750
catgtttgt ttgtttta aaaaaaa 1778

<210> 123

<211> 294

<212> PRT

<213> Homo sapiens

<400> 123

Met Pro Arg Gly Asp Ser Glu Gln Val Arg Tyr Cys Ala Arg Phe
1 5 10 15

Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val
20 25 30

Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala
35 40 45

Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu
50 55 60

Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met
65 70 75

Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr
80 85 90

Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met
95 100 105

Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr
110 115 120

Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr
125 130 135

Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys
140 145 150

Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys
155 160 165

Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly
170 175 180

Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn
185 190 195

Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val

200	205	210
Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile		
215	220	225
Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly		
230	235	240
Ile Leu Leu Pro Gln Phe Leu Gly Val Leu Leu Thr Leu Leu Tyr		
245	250	255
Ile Thr Arg Val Glu Asp Ile Ile Met Glu His Ser Val Thr Asp		
260	265	270
Gly Leu Leu Gly Pro Gly Ala Lys Pro Ser Val Glu Ala Ala Gly		
275	280	285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn		
290		

<210> 124

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 124

atcatctatt ccaccgtgtt ctggc 25

<210> 125

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gacagagtgc tccatgatga tgtcc 25

<210> 126

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

cctgtctgtg ggcattctatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127

<211> 1636

<212> DNA

<213> Homo sapiens

<400> 127

gaggagcggg ccgaggactc cagcgtgccc aggtctggca tctgcactt 50

gctgccctct gacacctggg aagatggccg gccctggac cttcaccctt 100

ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtcccac 150

tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200

agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250

agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300

ggtgaacacc gtctgaagc acatcatctg gctgaaggtc atcacagcta 350

acatcctcca gctgcaggtg aagccctcgg ccaatgacca ggagctgcta 400

gtcaagatcc ccttggaatc ggtggctgga ttcaacacgc ccctggtaaa 450

gaccatcgtg gaggccaca tgacgactga ggccaagcc accatccgca 500

tggacaccag tgcaagtggc cccacccgcc tggcctcag tgactgtgcc 550

accagccatg ggagcctgcg catccaactg ctgtataagc tctccttct 600

ggtgaacgcc ttagctaagc aggtcatgaa cctcctagt ccatccctgc 650

ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttcttcaat 700

ggcatgtatg cagacctcct gcagctgggtg aaggtgccca tttccctcag 750
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gaaaccagc tctcctgtct cccagtgaag acttgatgg cagccatcag 1550
ggaaggctgg gtccagctg ggagtatggg tgtgagctct atagaccatc 1600
cctctctgca atcaataaac actgcctgt gaaaaa 1636

<210> 128

<211> 484

<212> PRT

<213> Homo sapiens

<400> 128

Met Ala Gly Pro Trp Thr Phe Thr Leu Leu Cys Gly Leu Leu Ala
1 5 10 15

Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile
20 25 30

Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys
35 40 45

Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser
50 55 60

Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser
65 70 75

Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile
80 85 90

Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp
95 100 105

Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe
110 115 120

Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr
125 130 135

Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro
140 145 150

Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu
155 160 165

Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu
170 175 180

Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu
185 190 195

Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly
200 205 210

Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu
215 220 225

Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys
230 235 240

Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser
245 250 255

Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu
260 265 270

Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser
275 280 285

Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu
290 295 300

Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His
305 310 315

Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp
320 325 330

Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr
335 340 345

Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu
350 355 360

Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu
365 370 375

Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr
380 385 390

Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp
395 400 405

Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp
410 415 420

Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu

425	430	435
Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu		
440	445	450
Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys		
455	460	465
Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser		
470	475	480
Pro Val Ser Gln		

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

<400> 129
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 aaagaaggag atggtgttat ctgaaaaggt tagtcagctg atggaatgga 150
 ctaacaaaag acctgtaata agaatgaatg gagacaagtt ccgtcgcctt 200
 gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcaactgctct 250
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gtatattttg tattacctct tttttcaag tgatttaa atgttaatcat 1150
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<400> 130

Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val
1 5 10 15

Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln
20 25 30

Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met
35 40 45

Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
50 55 60

Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile
65 70 75

Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys
80 85 90

Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg
95 100 105

Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp
110 115 120

Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser
125 130 135

Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg
140 145 150

Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln
155 160 165

Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val
170 175 180

Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu
185 190 195

Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met
200 205 210

Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys
215 220 225

Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg
230 235 240

Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn
245 250 255

Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His
260 265 270

Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu
275 280 285

Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys

290	295	300
Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser		
305	310	315
Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr		
320	325	330
Ser Phe Leu Met Ser		
335		

<210> 131

<211> 2476

<212> DNA

<213> Homo sapiens

<400> 131

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cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200

cagccaaagc gcccaatgtg gtgctggtcg tgagcgactc cttcgatgga 250

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ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350

caatttgtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400

ttaacagaat cttggaataa ttttaagggt ctagatccaa attatacaac 450

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aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550

tggacaagag atgttgcttt ctactcaga caagaaggca ggcccatggt 600

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 aaaaaaaaa aaaaaaaaa aaaaaa 2476

<210> 132

<211> 536

<212> PRT

<213> Homo sapiens

<400> 132

Met	Leu	Leu	Leu	Trp	Val	Ser	Val	Val	Ala	Ala	Leu	Ala	Leu	Ala
1		5		10					15					

Val	Leu	Ala	Pro	Gly	Ala	Gly	Glu	Gln	Arg	Arg	Arg	Ala	Ala	Lys
		20			25				30					

Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg

35	40	45
Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile		
50	55	60
Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr		
65	70	75
Asn Ser Pro Ile Cys Cys Pro Ser Arg Ala Ala Met Trp Ser Gly		
80	85	90
Leu Phe Thr His Leu Thr Glu Ser Trp Asn Asn Phe Lys Gly Leu		
95	100	105
Asp Pro Asn Tyr Thr Thr Trp Met Asp Val Met Glu Arg His Gly		
110	115	120
Tyr Arg Thr Gln Lys Phe Gly Lys Leu Asp Tyr Thr Ser Gly His		
125	130	135
His Ser Ile Ser Asn Arg Val Glu Ala Trp Thr Arg Asp Val Ala		
140	145	150
Phe Leu Leu Arg Gln Glu Gly Arg Pro Met Val Asn Leu Ile Arg		
155	160	165
Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp Trp Gln Asn Thr		
170	175	180
Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile Asn Tyr Thr		
185	190	195
Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His Pro Tyr		
200	205	210
Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe His		
215	220	225
Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys		
230	235	240
Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr		
245	250	255

Tyr Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys
260 265 270

Glu Ile Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu
275 280 285

Thr Asp Ala Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu
290 295 300

Asp Leu Leu Gln Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly
305 310 315

Glu Leu Ala Met Glu His Arg Gln Phe Tyr Lys Met Ser Met Tyr
320 325 330

Glu Ala Ser Ala His Val Pro Leu Leu Met Met Gly Pro Gly Ile
335 340 345

Lys Ala Gly Leu Gln Val Ser Asn Val Val Ser Leu Val Asp Ile
350 355 360

Tyr Pro Thr Met Leu Asp Ile Ala Gly Ile Pro Leu Pro Gln Asn
365 370 375

Leu Ser Gly Tyr Ser Leu Leu Pro Leu Ser Ser Glu Thr Phe Lys
380 385 390

Asn Glu His Lys Val Lys Asn Leu His Pro Pro Trp Ile Leu Ser
395 400 405

Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr Tyr Met Leu Arg
410 415 420

Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly Ala Ser Ile
425 430 435

Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu Leu Thr
440 445 450

Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp Gln
455 460 465

Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val

470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile		
485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln		
500	505	510
Asp Trp Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln		
515	520	525
Trp Leu Lys Thr His Met Asn Pro Arg Ala Val		
530	535	

<210> 133

<211> 1475

<212> DNA

<213> Homo sapiens

<400> 133

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tcaaggagca agagcttcag cctgaagaca agggagcagt ccctgaagac 100

gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150

ctacatccta ggcttcttgg ggcttttggg cacactggtt gccatgctgc 200

tcccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250

gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300

catcacccag tgtgacatct atagcaccct tctgggcctg cccgctgaca 350

tccaggctgc ccaggccatg atggtgacat ccagtgcaat ctctccctg 400

gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

atcccagacc aaagacagag tggcggtagc aggtggagtc ttttcatcc 500

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ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600

tggagagget ctttacttgg gcattatttc ttccctgttc tcctgatag 650
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 tactacgatg cctaccaagc ccaacctctt gccacaagga gctctccaag 750
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 cagggtatgt gtgaagaacc agggggccaga gctgggggggt ggctgggtct 850
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 ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga 1000
 attgccaagg atgctcgcca tgccagcctt tctgtttcc tcaccttget 1050
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 ccccaaacc actaatcaca tccactgac tgacctctg tgatcaaaga 1200
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 actccacagt gtccagacta attgtgcat gaactgaaat aaaaccatcc 1400
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<210> 134

<211> 230

<212> PRT

<213> Homo sapiens

<400> 134

Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu

1	5	10	15
Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp			
20	25	30	
Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly			
35	40	45	
Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly			
50	55	60	
Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala			
65	70	75	
Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile			
80	85	90	
Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met Arg Cys Thr			
95	100	105	
Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala Val Ala			
110	115	120	
Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro			
125	130	135	
Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro			
140	145	150	
Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr			
155	160	165	
Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile			
170	175	180	
Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr			
185	190	195	
Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg			
200	205	210	
Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser			
215	220	225	

Leu Thr Gly Tyr Val
230

<210> 135
<211> 610
<212> DNA
<213> Homo sapiens

<400> 135
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agggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200
cgccatcgtg tccctgagcg agaccgcga atgtgggtccc cctgcacct 250
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<210> 136
<211> 119
<212> PRT
<213> Homo sapiens

<400> 136
Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
1 5 10 15

Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
20 25 30

Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
35 40 45

Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
50 55 60

Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
65 70 75

Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
80 85 90

Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
95 100 105

Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
110 115

<210> 137

<211> 771

<212> DNA

<213> Homo sapiens

<400> 137

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gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200

gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

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agaactgcga ctacgcccgg acctcgatg acaggctttg tcgcagtgtc 350

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tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagt 450

gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500

gacctgtctg aggcccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550

ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600

ggactctgaa ccctctgat gaccctatg gccaacatca acccggcacc 650

acccaaggc tggtgggga acccttcacc ctctgtgag attttccatc 700

atctcaagtt ctctctatc caggagcaaa gcacaggatc ataataaatt 750

tatgtacttt ataatgaaa a 771

<210> 138

<211> 110

<212> PRT

<213> Homo sapiens

<400> 138

Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys

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Ile Ser Arg Leu Leu Cys Ser His Gly Ala Pro Val Ala Pro Met

20 25 30

Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp

35 40 45

Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val

50 55 60

Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg

65 70 75

Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu

80 85 90

Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu

95 100 105

Cys Arg Ser Val Ser
110

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

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agacttctc ttgtaccac agtggctctg gggccaggcc tgctgcca 1600
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tggcctccgt gagcaaatgg tgtctgggc aatctgaggc caggacagat 1800
gttggccac cactggaga tggctgtgag ggaggtgggt ggggcctct 1850
gggaaggtga gtggagagg gcacctgcc cccgcctcc ccatcccta 1900
ctccactgc tcagcgggg ccattgcaag ggtgccacac aatgtctgt 1950

ccaccctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000

tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140

<211> 311

<212> PRT

<213> Homo sapiens

<400> 140

Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly

1 5 10 15

Ser Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val

20 25 30

Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro

35 40 45

Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val

50 55 60

Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser

65 70 75

Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg

80 85 90

Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln

95 100 105

Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu

110 115 120

Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn

125 130 135

Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu

140 145 150

Ile Arg His His His Ser Glu His Arg Val His Gly Ala Met Glu

155 160 165

Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val
170 175 180

Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr Ala Ala Ala
185 190 195

Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu
200 205 210

Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg
215 220 225

Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile
230 235 240

Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro
245 250 255

Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln
260 265 270

Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro
275 280 285

Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp
290 295 300

Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile
305 310

<210> 141

<211> 1732

<212> DNA

<213> Homo sapiens

<400> 141

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cttagacctc ccttctgccc ctctttcct gccaccgct gcttctggc 150

ccttctccga ccccgctcta gcagcagacc tcctggggtc tgtgggtga 200

tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgact 250
ccgctcccgg accagcggcc tgacctggg gaaaggatgg ttcccagagt 300
gagggtctc tcctcttgc tgggactgc gctgcttg ttccccctgg 350
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agatactccc ccggcgagag ctggcacccc tacttgagc cacaaggcct 450
gatgtactgc ctgcgtgta cctgtcaga gggcgcccat gtgagttgtt 500
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cagtcgtcc atggggtgag acatcctcag gatccatgtt ccagtgatgc 900
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cgggaagacg tactcccag gggaggtgtg gcacccggcc ttccgtgctt 1100
tcggccccct gccctgcatc ctatgcacct gtgaggatgg ccgccaggac 1150
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gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300

ctcgtccaca catcggtatc cccaagccca gacaacctgc gtcgctttgc 1350
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aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac 1550
gaaggtcact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600
ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650
gatatgagct gtataattgt tgttattata tattaataaa taagaagttg 1700
cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142

<211> 451

<212> PRT

<213> Homo sapiens

<400> 142

Met Val Pro Glu Val Arg Val Leu Ser Ser Leu Leu Gly Leu Ala

1 5 10 15

Leu Leu Trp Phe Pro Leu Asp Ser His Ala Arg Ala Arg Pro Asp

20 25 30

Met Phe Cys Leu Phe His Gly Lys Arg Tyr Ser Pro Gly Glu Ser

35 40 45

Trp His Pro Tyr Leu Glu Pro Gln Gly Leu Met Tyr Cys Leu Arg

50 55 60

Cys Thr Cys Ser Glu Gly Ala His Val Ser Cys Tyr Arg Leu His

65 70 75

Cys Pro Pro Val His Cys Pro Gln Pro Val Thr Glu Pro Gln Gln

80 85 90

Cys Cys Pro Lys Cys Val Glu Pro His Thr Pro Ser Gly Leu Arg

95	100	105
Ala Pro Pro Lys Ser Cys Gln His Asn Gly Thr Met Tyr Gln His		
110	115	120
Gly Glu Ile Phe Ser Ala His Glu Leu Phe Pro Ser Arg Leu Pro		
125	130	135
Asn Gln Cys Val Leu Cys Ser Cys Thr Glu Gly Gln Ile Tyr Cys		
140	145	150
Gly Leu Thr Thr Cys Pro Glu Pro Gly Cys Pro Ala Pro Leu Pro		
155	160	165
Leu Pro Asp Ser Cys Cys Gln Ala Cys Lys Asp Glu Ala Ser Glu		
170	175	180
Gln Ser Asp Glu Glu Asp Ser Val Gln Ser Leu His Gly Val Arg		
185	190	195
His Pro Gln Asp Pro Cys Ser Ser Asp Ala Gly Arg Lys Arg Gly		
200	205	210
Pro Gly Thr Pro Ala Pro Thr Gly Leu Ser Ala Pro Leu Ser Phe		
215	220	225
Ile Pro Arg His Phe Arg Pro Lys Gly Ala Gly Ser Thr Thr Val		
230	235	240
Lys Ile Val Leu Lys Glu Lys His Lys Lys Ala Cys Val His Gly		
245	250	255
Gly Lys Thr Tyr Ser His Gly Glu Val Trp His Pro Ala Phe Arg		
260	265	270
Ala Phe Gly Pro Leu Pro Cys Ile Leu Cys Thr Cys Glu Asp Gly		
275	280	285
Arg Gln Asp Cys Gln Arg Val Thr Cys Pro Thr Glu Tyr Pro Cys		
290	295	300
Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro		
305	310	315

Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg
 320 325 330
 Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser
 335 340 345
 Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala
 350 355 360
 Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu
 365 370 375
 Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His
 380 385 390
 Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala
 395 400 405
 Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro
 410 415 420
 Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala
 425 430 435
 Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys
 440 445 450

Thr

<210> 143

<211> 693

<212> DNA

<213> Homo sapiens

<400> 143

ctagcctgcg ccaaggggta gtgagaccgc gcggcaacag cttgcggctg 50

cggggagctc ccgtgggcgc tccgctggct gtgcaggcgg ccatggattc 100

cttgcggaat atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150

tgggctacgc gctcctcgtt atcgtgaccc cgggagagcg gcggaagcag 200

gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250
 ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300
 cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350
 ggcgccagcg ggaggtcacc gtgagaccgg acttgcttcc gtgggcgccg 400
 gaccttggtt tgggcgcagg aatccgaggc agcctttctc ctctgtgggc 450
 ccagcggaga gtccggaccg agataccatg ccaggactct ccggggctct 500
 gtgagctgcc gtcgggtgag cacgtttccc ccaaacctg gactgactgc 550
 tttaaggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600
 aactgaaaga accaataaaa tcatttctt ccaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144

<211> 93

<212> PRT

<213> Homo sapiens

<400> 144

Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
 1 5 10 15

Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
 20 25 30

Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
 35 40 45

Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
 50 55 60

Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
 65 70 75

Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
 80 85 90

Arg Ser Pro

<210> 145

<211> 1883

<212> DNA

<213> Homo sapiens

<400> 145

caggagagaa ggcaccgccc ccaccccgcc tccaaagcta accctcgggc 50

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caggctgccca tggggcccag caccctctc ctcacttctg tccttttctc 150

atggtcggga cccctccaag gacagcagca ccaccttgtg gagtacatgg 200

aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250

agtagtcggc atgtctctga gctgcgggac ttcaagaaca agatgctgcc 300

actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350

acaccatctc cgggagagtg gatcgtcttg agcgggaggt agactatctg 400

gagaccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450

tggaggccct gggaccaaag gcaagggaag aaggaatgag aagtacgata 500

tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550

ctgaagcgat ttggtggccc agctggtcta tggaccaagg atccactggg 600

gcaaacagag aagatctacg tgtagatgg gacacagaat gacacagcct 650

ttgtcttccc aaggctgcgt gacttcaccc ttgcatggc tgcccggaaa 700

gcttcccag tccgggtgcc ctcccctgg gtaggcacag ggcagctggt 750

atatggtggc ttcttttatt ttgctcggag gcctcctgga agacctggtg 800

gagggtgtga gatggagaac actttgcagc taatcaaatt ccacctggca 850

aaccgaacag tggatggacag ctacgtattc ccagcagagg ggctgatccc 900
cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950
aaggtctttg ggctgtctat gccacccggg aggatgacag gcacttgtgt 1000
ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050
accatgtccc agagagaatg ctgaggctgc ctttgcac tgtagggacc 1100
tctatgtcgt ctataacacc cgtctgcca gtcggggccg catccagtgc 1150
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aacaggactt tctccacatt gtttgtatt gcaacattt gcattaaaag 1800
gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp
1 5 10 15

Ser Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met
20 25 30

Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln
35 40 45

Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn
50 55 60

Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala
65 70 75

Leu Arg Thr Glu Ala Asp Thr Ile Ser Gly Arg Val Asp Arg Leu
80 85 90

Glu Arg Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro
95 100 105

Cys Val Glu Phe Asp Glu Lys Val Thr Gly Gly Pro Gly Thr Lys
110 115 120

Gly Lys Gly Arg Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys
125 130 135

Gly Tyr Thr Ile Ser Gln Val Arg Ser Met Lys Ile Leu Lys Arg
140 145 150

Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys Asp Pro Leu Gly Gln
155 160 165

Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln Asn Asp Thr Ala
170 175 180

Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala Met Ala Ala
185 190 195

Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val Gly Thr
200 205 210

Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg Pro
215 220 225

Pro Gly Arg Pro Gly Gly Gly Gly Glu Met Glu Asn Thr Leu Gln
230 235 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser
245 250 255

Val Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala
260 265 270

Asp Thr Tyr Ile Asp Leu Val Ala Asp Glu Glu Gly Leu Trp Ala
275 280 285

Val Tyr Ala Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys
290 295 300

Leu Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro
305 310 315

Cys Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys Gly Thr
320 325 330

Leu Tyr Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg Ile
335 340 345

Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala
350 355 360

Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu
365 370 375

Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly
380 385 390

Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu
395 400 405

Val

<210> 147

<211> 2052

<212> DNA

<213> Homo sapiens

<400> 147

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ccgctcacgc agagcctctc cgtggcttcc gcacctgag cattaggcca 100

gttctctct tctctctaat ccatccgtca cctctctgt catccgttc 150

catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200

ttggttctga gtctctcaa gctgggatca gggcagtggc aggtgtttgg 250

gccagacaag cctgtccagg ccttgggtggg ggaggacgca gcattctct 300

gtttctgtc tcctaagacc aatgcagagg ccatggaagt gcggttctc 350

aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400

gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450

attctattgc ggaggggcgc atctctctga ggctggaaaa cattactgtg 500

ttggatgctg gcctctatgg gtgcaggatt agtcccagt ctactacca 550

gaaggccatc tgggagctac aggtgtcagc actgggctca gttctctca 600

ttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtc 650

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ggatttgtcc acagactcca ggacaaacag agacatgcat ggcctgttg 750

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tccatgcggc atgtctatct gagccgagag gtggaatcca gggtacagat 850

aggagatacc ttttcgagc ctatctgtg gcacctggct accaaagtac 900

tggaataact ctgctgtggc ctatTTTTg gcattgttgg actgaagatt 950
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aaagcacgga caggcagaat tgagagacgc ccggaacac gcagtggagg 1050
tgactctgga tccagagacg gctcaccga agctctgcgt ttctgatctg 1100
aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150
gagatttaca aggaagagtg tgggtggcttc tcagagtttc caagcaggga 1200
aacattactg ggaggtggac ggaggacaca ataaaagggtg gcgcgtggga 1250
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cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtattca 1350
cattaaatcc ccgtttatc agcgtcttc ccaggacccc acctacaaaa 1400
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caaccacgcc ctctctccc aggggtgaaa ttaggatga atcacatccc 1700
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cattacattt agtttgcct cactccatct ggctaagtga tcttgaata 1900
ccacctctca ggtgaagaac cgtcaggaat tccatctca caggctgtgg 1950
ttagattaa gtgacaagg aatgtgaata atgcttagat cttattgatg 2000

acagagtgtg tccaatggt ttgttcatta tattacactt tcagtaaaaa 2050

aa 2052

<210> 148

<211> 500

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly

1 5 10 15

Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala

20 25 30

Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys

35 40 45

Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe

50 55 60

Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe

65 70 75

Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp

80 85 90

Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr

95 100 105

Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser

110 115 120

Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly

125 130 135

Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile

140 145 150

Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala

155 160 165

Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg
170 175 180

Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu
185 190 195

Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His
200 205 210

Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp
215 220 225

Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu
230 235 240

Gly Ile Leu Cys Cys Gly Leu Phe Phe Gly Ile Val Gly Leu Lys
245 250 255

Ile Phe Phe Ser Lys Phe Gln Trp Lys Ile Gln Ala Glu Leu Asp
260 265 270

Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys
275 280 285

His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys
290 295 300

Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro
305 310 315

Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val
320 325 330

Val Ala Ser Gln Ser Phe Gln Ala Gly Lys His Tyr Trp Glu Val
335 340 345

Asp Gly Gly His Asn Lys Arg Trp Arg Val Gly Val Cys Arg Asp
350 355 360

Asp Val Asp Arg Arg Lys Glu Tyr Val Thr Leu Ser Pro Asp His
365 370 375

Gly Tyr Trp Val Leu Arg Leu Asn Gly Glu His Leu Tyr Phe Thr

380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe Pro Arg Thr Pro Pro Thr		
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu Cys Gly Thr Ile Ser Phe		
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile Tyr Thr Leu Thr Cys Arg		
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile Glu Tyr Pro Ser Tyr Asn		
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile Cys Pro Val Thr Gln Glu		
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg Ala Ser Ala Ile Pro Glu		
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln Ala Thr Thr Pro Phe Leu		
485	490	495
Pro Arg Gly Glu Met		
500		

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 149

gcgtggtcca cctctacagg gacg 24

<210> 150

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 150

ggaactgacc cagtgtgac acc 23

<210> 151

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 151

gcagatgccca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152

<211> 2294

<212> DNA

<213> Homo sapiens

<400> 152

gcgatggtgc gcccgggtgc ggtggcggcg gcggttgcgg aggccttcctt 50

ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100

aatgaatggc ggagccgagc gcgcatgag gagcctgccg agcctgggcg 150

gcctcgccct gttgtgctgc gccgccgccg ccgccgccgt cgcctcagcc 200

gcctcggcgg ggaatgtcac cgttggcggc ggggccgcgg ggcaggtgga 250

cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300

gggcgacggc tcccacggcc caggccccga ggaccgggcc cccgcgcgcc 350

accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400

caccctctt tggcgactg ctggaccctc ttccaccacc ttccagcgc 450

cgtcggccc ctgccgacc accctccgg cggcggaacg cacttcgacc 500

accttcagg cgccgaccag acccgcccg accaccctt cgacgaccac 550

tgccccggcg ccgaccaccc ctgtagcgac caccgtaccg gcgcccacga 600
ctccccggac ccgaccccc gatctcccca gcagcagcaa cagcagcgtc 650
ctccccaccc cacctgccac cgaggccccc tcttcgcctc ctccagagta 700
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<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met Arg Ser Leu Pro Ser Leu Gly Gly Leu Ala Leu Leu Cys Cys

1 5 10 15

Ala Ala Ala Ala Ala Ala Val Ala Ser Ala Ala Ser Ala Gly Asn

20 25 30

Val Thr Gly Gly Gly Gly Ala Ala Gly Gln Val Asp Ala Ser Pro

35 40 45

Gly Pro Gly Leu Arg Gly Glu Pro Ser His Pro Phe Pro Arg Ala

50 55 60

Thr Ala Pro Thr Ala Gln Ala Pro Arg Thr Gly Pro Pro Arg Ala
65 70 75

Thr Val His Arg Pro Leu Ala Ala Thr Ser Pro Ala Gln Ser Pro
80 85 90

Glu Thr Thr Pro Leu Trp Ala Thr Ala Gly Pro Ser Ser Thr Thr
95 100 105

Phe Gln Ala Pro Leu Gly Pro Ser Pro Thr Thr Pro Pro Ala Ala
110 115 120

Glu Arg Thr Ser Thr Thr Ser Gln Ala Pro Thr Arg Pro Ala Pro
125 130 135

Thr Thr Leu Ser Thr Thr Thr Gly Pro Ala Pro Thr Thr Pro Val
140 145 150

Ala Thr Thr Val Pro Ala Pro Thr Thr Pro Arg Thr Pro Thr Pro
155 160 165

Asp Leu Pro Ser Ser Ser Asn Ser Ser Val Leu Pro Thr Pro Pro
170 175 180

Ala Thr Glu Ala Pro Ser Ser Pro Pro Pro Glu Tyr Val Cys Asn
185 190 195

Cys Ser Val Val Gly Ser Leu Asn Val Asn Arg Cys Asn Gln Thr
200 205 210

Thr Gly Gln Cys Glu Cys Arg Pro Gly Tyr Gln Gly Leu His Cys
215 220 225

Glu Thr Cys Lys Glu Gly Phe Tyr Leu Asn Tyr Thr Ser Gly Leu
230 235 240

Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro
245 250 255

Cys Asn Arg

<210> 154

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 154

aactgctctg tgggtggaag cctg 24

<210> 155

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 155

cagtcacatg gctgacagac ccac 24

<210> 156

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 156

aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157

<211> 689

<212> DNA

<213> Homo sapiens

<400> 157

tgcggcgcag ttagacctg ggaggatggg cggcctgctg ctggctgctt 50

ttctggcttt ggtctcggtg cccagggccccc aggccgtgtg gttgggaaga 100

ctggacctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150

ccgggaaaag ggctttgcca tggagaagga catgaagaac gtcgtggggg 200

tggtggtgac cctcactcca gaaaacaacc tgcggacgct gtctctcag 250

cacgggctgg gaggggtgta ccagagtgtc atggacctga taaagcгаа 300

ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350

tgtggccac caacttcaga gactatcca tcatttcac tcagctggag 400

ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450

agccagccag gaggccatgg ggctcttcac caagtgagc aggagcctgg 500

gcttcctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550

cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgcccaca 600

gggtcctgtg acctcgгca gtgtccacc acctcgctca gcggctcccg 650

gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158

<211> 163

<212> PRT

<213> Homo sapiens

<400> 158

Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val

1 5 10 15

Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln

20 25 30

Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys

35 40 45

Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val

50 55 60

Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln

65 70 75

His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
80 85 90

Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu
95 100 105

Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile
110 115 120

Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu
125 130 135

Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu
140 145 150

Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe Leu Ser Gln
155 160

<210> 159

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 159

aacagacgtt ccctcgcggc cctggcacct ctaaccccag acatgctgct 50

gctgctgctg cccctgctct gggggaggga gagggcggaa ggacagacaa 100

gtaaactgct gacgatgcag agttccgtga cggtgcagga aggcctgtgt 150

gtccatgtgc cctgctcctt ctctacccc tcgcatggct ggatttacc 200

tggcccagta gttcatggct actggtccg ggaaggggcc aatacagacc 250

aggatgctcc agtggccaca aacaaccag ctcgggcagt gtgggaggag 300

actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350

cctgagcatc agagatgcc aagaagtga tgcggggaga tacttcttc 400

gtatggagaa aggaagtata aaatggaatt ataaacatca ccggtctct 450

gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500

cctggagtcc ggctgcccc agaattctgac ctgctctgtg ccctgggcct 550
gtgagcaggg gacaccccct atgatctcct ggataggac ctccgtgtcc 600
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gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctaccgcct 750
cagaactga ccatgactgt ctccaagga gacggcacag tatccacagt 800
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tgattctgt agaattaaca gccctcaacg tgatgagcta tgataacact 1550
atgaattatg tcagagtga aaagcacaca ggcttagag tcaaagtatc 1600

tcaaacctga atccacactg tgccctccct tttatTTTT taactaaaag 1650

acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met Leu Leu Leu Leu Leu Pro Leu Leu Trp Gly Arg Glu Arg Ala

1 5 10 15

Glu Gly Gln Thr Ser Lys Leu Leu Thr Met Gln Ser Ser Val Thr

20 25 30

Val Gln Glu Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr

35 40 45

Pro Ser His Gly Trp Ile Tyr Pro Gly Pro Val Val His Gly Tyr

50 55 60

Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln Asp Ala Pro Val Ala

65 70 75

Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu Thr Arg Asp Arg

80 85 90

Phe His Leu Leu Gly Asp Pro His Thr Lys Asn Cys Thr Leu Ser

95 100 105

Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg

110 115 120

Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu

125 130 135

Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile

140 145 150

Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser

155 160 165

Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp
170 175 180

Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser
185 190 195

Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser
200 205 210

Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn
215 220 225

Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr
230 235 240

Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly
245 250 255

Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu
260 265 270

Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu
275 280 285

Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser
290 295 300

Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala
305 310 315

Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln
320 325 330

Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val
335 340 345

Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe
350 355 360

Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys
365 370 375

Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu

380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr		
395	400	405
Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala		
410	415	420
Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser		
425	430	435
Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu		
440	445	450
Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg		
455	460	

<210> 161

<211> 739

<212> DNA

<213> Homo sapiens

<400> 161

gacgccagtg gacctgccga ggtcggcagc acagagctct ggagatgaag 50

accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgccttcac 100

cctggaggag gaggatatca caggacacgt gtacgtgaag gccatggtgg 150

tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagtg 200

aaggtgacag ccctgggcgg tgggaagttg gaagccacgt tcaccttcac 250

gaggaggagat cgggtgatcc agaagaaaat cctgatgcgg aagacggagg 300

agcctggcaa atacagcgc tatgggggca ggaagctcat gtacctgcag 350

gagctgcccc ggagggacca ctacatctt tactgcaaag accagcacca 400

tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450

accgggaggc cctggaagaa tttaagaaat tggtcagcg caagggactc 500

tggaggagg acattttcac gccctgcag acgggaagct gcgtcccga 550

acactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600

acacagagcc cggaccacct ggacctaccc tccagccatg acccttcct 650

gtccccccc acctgactcc aaataaagtc ctttcccc aaaaaaaaaa 700

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162

<211> 170

<212> PRT

<213> Homo sapiens

<400> 162

Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala

1 5 10 15

Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20 25 30

Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg

35 40 45

Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly

50 55 60

Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile

65 70 75

Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu Pro Gly Lys Tyr

80 85 90

Ser Ala Tyr Gly Gly Arg Lys Leu Met Tyr Leu Gln Glu Leu Pro

95 100 105

Arg Arg Asp His Tyr Ile Phe Tyr Cys Lys Asp Gln His His Gly

110 115 120

Gly Leu Leu His Met Gly Lys Leu Val Gly Arg Asn Ser Asp Thr

125 130 135

Asn Arg Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln Arg Lys
140 145 150

Gly Leu Ser Glu Glu Asp Ile Phe Thr Pro Leu Gln Thr Gly Ser
155 160 165

Cys Val Pro Glu His
170

<210> 163

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

ggagatgaag accctgttcc tg 22

<210> 164

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164

ggagatgaag accctgttcc tgggtg 26

<210> 165

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 165

gtcctccgga aagtccttat c 21

<210> 166

<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 166
gcctagtgtt cggaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 167
caggacctg gtacgtgaag gccatggtg tcgataagga cttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 168
ctgtcctca ccctggagga ggaggatc acaggacct ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169
gtccgcaga tcagaggtt gaggtggctg cgggactgga agtcacggg 50

cagaggtctc acagcagcca aggaacctgg ggcccgtcc tccccctcc 100

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggtt 150

gtagggggag agaccaggat catcaagggg ttcgagtga agcctcactc 200
ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtgggg 250
cgacgtcat cgtccccaga tggctcctga cagcagccca ctgcctcaag 300
ccccgtaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350
ctgtgagcag acccggacag ccaactgagtc ctccccac cccggettca 400
acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450
atggcatcgc cagtctccat cacctgggct gtgcgacccc tcacctctc 500
ctcacgtgt gtcactgtg gcaccagctg cctcatttc ggctggggca 550
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cacagacacc atggtgtgtg ccagcgtga ggaagggggc aaggactcct 700
gccaggggta ctccgggggc cctctggtct gtaaccagtc tctcaaggc 750
attatctct ggggccagga tccgtgtgcg atcacccgaa agcctggtgt 800
ctacacgaaa gtctgcaaat atgtggactg gatccaggag acgatgaaga 850
acaattagac tggaccacc caccacagcc catcacctc cattccact 900
tggtgtttg ttcctgtca ctctgttaat aagaaaccct aagccaagac 950
cctctacgaa cattctttg gcctcctgga ctacaggaga tgctgtcact 1000
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tgtatcccca gcccacaaaga cagctcctgg ccatatatca aggtttcaat 1150
aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
aaaa 1204

<210> 170

<211> 250

<212> PRT

<213> Homo sapiens

<400> 170

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
1 5 10 15

Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro
20 25 30

His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu
35 40 45

Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala
50 55 60

Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His
65 70 75

Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr
80 85 90

Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys
95 100 105

Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro Val
110 115 120

Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys
125 130 135

Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr
140 145 150

Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn
155 160 165

Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly
170 175 180

Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly Gly

185 190 195

Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn
200 205 210

Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala
215 220 225

Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val
230 235 240

Asp Trp Ile Gln Glu Thr Met Lys Asn Asn
245 250

<210> 171

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

ggctgcggga ctggaagtca tcggg 25

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

ctccaggcca tgaggattct gcag 24

<210> 173

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 173
cctctggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 174
tctgtgatgt tgccggggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 175
cgtgtagaca ccaggcttgc gggcg 25

<210> 176
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 176
cccttgatga tcctgggc 18

<210> 177
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 178

gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttctttat ctgtggggcc ttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaat atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaagg agacctacta aatgccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atggtttgtt cttggtgttg ggcaagtc 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca ttgcatacg gaaaggaagg ctatgcagaa 400

ggcaagattc caccgatgc tacattgatt ttgagattg aactttatgc 450

tgtgacaaa ggaccacgga gcattgagac atttaacaa atagacatgg 500

acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550

gaatttgaaa aagatgagaa gccacgtgac aagtcatac aggatgcagt 600

tttagaagat attttaaga agaatgacca tgatggatgat ggcttcattt 650

ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700

atttctactt tttttttta gctatttact gtactttatg tataaaacaa 750

agtcactttt ctccaagttg tatttgctat ttttcccta tgagaagata 800

ttttagatc cccaatacat tgattttggg ataataaatg tgaggctgtt 850

ttgcaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900

aaaaaaaa 907

<210> 180

<211> 222

<212> PRT

<213> Homo sapiens

<400> 180

Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe

1 5 10 15

Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu

20 25 30

Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn

35 40 45

Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr

50 55 60

Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg

65 70 75

Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly

80 85 90

Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro

95 100 105

Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly

110 115 120

Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu
125 130 135

Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser
140 145 150

Ile Glu Thr Phe Lys Gln Ile Asp Met Asp Asn Asp Arg Gln Leu
155 160 165

Ser Lys Ala Glu Ile Asn Leu Tyr Leu Gln Arg Glu Phe Glu Lys
170 175 180

Asp Glu Lys Pro Arg Asp Lys Ser Tyr Gln Asp Ala Val Leu Glu
185 190 195

Asp Ile Phe Lys Lys Asn Asp His Asp Gly Asp Gly Phe Ile Ser
200 205 210

Pro Lys Glu Tyr Asn Val Tyr Gln His Asp Glu Leu
215 220

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

gtgttctgct ggagccgatg cc 22

<210> 182

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 182

gacatggaca atgacagg 18

<210> 183

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 183

cctttcagga ttaggag 18

<210> 184

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184

gatgtctgcc accccaag 18

<210> 185

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 185

gcacacctgat atgactgtc acgtggc 27

<210> 186

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 186

tacaagaggg aagaggagtt gcac 24

<210> 187

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 187

gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50

cc 52

<210> 188

<211> 573

<212> DNA

<213> Homo sapiens

<400> 188

cagaaatgca gggaccattg cttcttcag gcctctgctt tctgctgagc 50

ctctttggag ctgtgactca gaaaacaaa acttctgtg ctaagtgcc 100

cccaaatgct tctgtgtca ataactca ctgcacctgc aacctggat 150

atattcttg atctgggcag aaactattca cattccccctt ggagacatgt 200

aagccaggc atggtggctc gcgcctgtaa tcccagttct ttggaagcc 250

aaggcagtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300

atagtgaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350

ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400

cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450

ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500

ttctgtttc atttcgcgac tgccctctca gtgtttctg ggatcccctc 550

ccaaataaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser
1 5 10 15

Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
20 25 30

Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
35 40 45

Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
50 55 60

Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
65 70

<210> 190

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 190

agggaccatt gcttcttcca ggcc 24

<210> 191

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 191

cgttacatgt ctccaagggg aatg 24

<210> 192

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 192

cctgtgctaa gtgccccca aatgttctct gtgtcaataa cactcactgc 50

<210> 193

<211> 1091

<212> DNA

<213> Homo sapiens

<400> 193

caagcaggtc atccccttgg tgaccttcaa agagaagcag agagggcaga 50

ggtggggggc acagggaaag ggtgacctct gagattcccc ttccccca 100

gactttggaa gtgaccacc atggggctca gcatctttt gctcctgtgt 150

gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200

gtgtgggcgt aactcacagc cgtggcagggt ggggctgttt gagggcacca 250

gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300

gctcactgca gcggcagcag gtactgggtg cgctggggg aacacagcct 350

cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400

cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450

ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccct 500

gcccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550

gctggggcat caccaaccac ccacggaacc cattcccga tctgtccag 600

tgctcaacc tctccatgt ctccatgcc acctgccatg gtgtgtatcc 650

cgggagaatc acgagcaaca tgggtgtgtgc aggcggcgtc ccggggcagg 700
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 ccctagctcc actctgttg gcctgggaac ttcttgaac tttaactcct 1000
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 tggataaat ataatgaag gaggggcaaa aaaaaaaaa a 1091

<210> 194

<211> 248

<212> PRT

<213> Homo sapiens

<400> 194

Met Gly Leu Ser Ile Phe Leu Leu Leu Cys Val Leu Gly Leu Ser

1 5 10 15

Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg

20 25 30

Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu

35 40 45

Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala

50 55 60

Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His

65 70 75

Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly

80 85 90

Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His

95	100	105
Glu His Asp Leu Arg Leu Arg Leu Arg Leu Pro Val Arg Val		
110	115	120
Thr Ser Ser Val Gln Pro Leu Pro Leu Pro Asn Asp Cys Ala Thr		
125	130	135
Ala Gly Thr Glu Cys His Val Ser Gly Trp Gly Ile Thr Asn His		
140	145	150
Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln Cys Leu Asn Leu Ser		
155	160	165
Ile Val Ser His Ala Thr Cys His Gly Val Tyr Pro Gly Arg Ile		
170	175	180
Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly Gln Asp Ala		
185	190	195
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val Leu		
200	205	210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp		
215	220	225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp		
230	235	240
Ile Arg Met Ile Met Arg Asn Asn		
245		

<210> 195

<211> 1485

<212> DNA

<213> Homo sapiens

<400> 195

gcggccacac gcagctagcc ggagcccgga ccaggcgcct gtgcctcctc 50

ctcgtccctc gccgcgtccg cgaagcctgg agccggcggg agccccgcgc 100

tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgttc 150

ggcttgctca aagccccgca ggagaggagg ctggccgaga tcaaccggga 200
gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250
tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350
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aagtcagcag cactggtaag ccaagactga gaaatacaag gttgctgtc 1450

tgacccaat ctgcttgaat aaaaaaaaaa aaaaa 1485

<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

Met Ser Gly Glu Leu Ser Asn Arg Phe Gln Gly Gly Lys Ala Phe

1 5 10 15

Gly Leu Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn

20 25 30

Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu

35 40 45

Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp

50 55 60

Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met

65 70 75

Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys

80 85 90

Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr

95 100 105

Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu

110 115 120

Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro

125 130 135

Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro
140 145 150

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

<400> 197

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gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200

gtcccgctgc cagcgtggac tgccacgggc tgggcctccg cgcggttct 250

cggggcatcc cccgcaacgc tgagcgcctt gacctggaca gaaataatat 300

caccaggatc accaagatgg acttcgctgg gctcaagaac ctccgagtct 350

tgcatttga agacaaccag gtcagcgtca tcgagagagg cgccttcag 400

gacctgaagc agctagagcg actgcgcctg aacaagaata agctgcaagt 450

ccttcagaa ttgctttcc agagcacgcc gaagtcacc agactagatt 500

tgagtgaata ccagatccag gggatcccga ggaaggcgtt ccgcggcatc 550

accgatgtga agaacctgca actggacaac aaccacatca gctgcattga 600

agatggagcc ttccgagcgc tgcgcgattt ggagatcctt accctcaaca 650

acaacaacat cagtcgcac ctggtcacca gcttcaacca catgccgaag 700

atccgaactc tgcgcctcca ctccaaccac ctctactgcg actgccacct 750

ggcctggctc tcggattggc tgcgacagcg acggacagtt ggccagtta 800

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<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

Met	Ala	Pro	Gly	Trp	Ala	Gly	Val	Gly	Ala	Ala	Val	Arg	Ala	Arg
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Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Ser	Val	Leu	Ser	Gly	Pro	Pro
		20		25		30								

Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val
		35		40		45								

Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro
50 55 60

Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg
65 70 75

Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu
80 85 90

His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe
95 100 105

Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys
110 115 120

Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu
125 130 135

Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg
140 145 150

Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp
155 160 165

Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu
170 175 180

Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Asn Ile Ser Arg
185 190 195

Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu
200 205 210

Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp
215 220 225

Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr
230 235 240

Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp
245 250 255

Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro

260	265	270
Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr		
275	280	285
Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu		
290	295	300
Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu		
305	310	315
Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr		
320	325	330
Lys Lys Leu Lys Arg Ile Asp Ile Ser Lys Asn Gln Ile Ser Asp		
335	340	345
Ile Ala Pro Asp Ala Phe Gln Gly Leu Lys Ser Leu Thr Ser Leu		
350	355	360
Val Leu Tyr Gly Asn Lys Ile Thr Glu Ile Ala Lys Gly Leu Phe		
365	370	375
Asp Gly Leu Val Ser Leu Gln Leu Leu Leu Leu Asn Ala Asn Lys		
380	385	390
Ile Asn Cys Leu Arg Val Asn Thr Phe Gln Asp Leu Gln Asn Leu		
395	400	405
Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ser Lys		
410	415	420
Gly Leu Phe Ala Pro Leu Gln Ser Ile Gln Thr Leu His Leu Ala		
425	430	435
Gln Asn Pro Phe Val Cys Asp Cys His Leu Lys Trp Leu Ala Asp		
440	445	450
Tyr Leu Gln Asp Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Ser		
455	460	465
Ser Pro Arg Arg Leu Ala Asn Lys Arg Ile Ser Gln Ile Lys Ser		
470	475	480

Lys Lys Phe Arg Cys Ser Gly Ser Glu Asp Tyr Arg Ser Arg Phe			
485	490	495	
Ser Ser Glu Cys Phe Met Asp Leu Val Cys Pro Glu Lys Cys Arg			
500	505	510	
Cys Glu Gly Thr Ile Val Asp Cys Ser Asn Gln Lys Leu Val Arg			
515	520	525	
Ile Pro Ser His Leu Pro Glu Tyr Val Thr Asp Leu Arg Leu Asn			
530	535	540	
Asp Asn Glu Val Ser Val Leu Glu Ala Thr Gly Ile Phe Lys Lys			
545	550	555	
Leu Pro Asn Leu Arg Lys Ile Asn Leu Ser Asn Asn Lys Ile Lys			
560	565	570	
Glu Val Arg Glu Gly Ala Phe Asp Gly Ala Ala Ser Val Gln Glu			
575	580	585	
Leu Met Leu Thr Gly Asn Gln Leu Glu Thr Val His Gly Arg Val			
590	595	600	
Phe Arg Gly Leu Ser Gly Leu Lys Thr Leu Met Leu Arg Ser Asn			
605	610	615	
Leu Ile Ser Cys Val Ser Asn Asp Thr Phe Ala Gly Leu Ser Ser			
620	625	630	
Val Arg Leu Leu Ser Leu Tyr Asp Asn Arg Ile Thr Thr Ile Thr			
635	640	645	
Pro Gly Ala Phe Thr Thr Leu Val Ser Leu Ser Thr Ile Asn Leu			
650	655	660	
Leu Ser Asn Pro Phe Asn Cys Asn Cys His Leu Ala Trp Leu Gly			
665	670	675	
Lys Trp Leu Arg Lys Arg Arg Ile Val Ser Gly Asn Pro Arg Cys			
680	685	690	
Gln Lys Pro Phe Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala			

695	700	705
Ile Gln Asp Phe Thr Cys Asp Gly Asn Glu Glu Ser Ser Cys Gln		
710	715	720
Leu Ser Pro Arg Cys Pro Glu Gln Cys Thr Cys Met Glu Thr Val		
725	730	735
Val Arg Cys Ser Asn Lys Gly Leu Arg Ala Leu Pro Arg Gly Met		
740	745	750
Pro Lys Asp Val Thr Glu Leu Tyr Leu Glu Gly Asn His Leu Thr		
755	760	765
Ala Val Pro Arg Glu Leu Ser Ala Leu Arg His Leu Thr Leu Ile		
770	775	780
Asp Leu Ser Asn Asn Ser Ile Ser Met Leu Thr Asn Tyr Thr Phe		
785	790	795
Ser Asn Met Ser His Leu Ser Thr Leu Ile Leu Ser Tyr Asn Arg		
800	805	810
Leu Arg Cys Ile Pro Val His Ala Phe Asn Gly Leu Arg Ser Leu		
815	820	825
Arg Val Leu Thr Leu His Gly Asn Asp Ile Ser Ser Val Pro Glu		
830	835	840
Gly Ser Phe Asn Asp Leu Thr Ser Leu Ser His Leu Ala Leu Gly		
845	850	855
Thr Asn Pro Leu His Cys Asp Cys Ser Leu Arg Trp Leu Ser Glu		
860	865	870
Trp Val Lys Ala Gly Tyr Lys Glu Pro Gly Ile Ala Arg Cys Ser		
875	880	885
Ser Pro Glu Pro Met Ala Asp Arg Leu Leu Leu Thr Thr Pro Thr		
890	895	900
His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn Ile Val Ala		
905	910	915

Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn Gly Thr
920 925 930

Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro Tyr
935 940 945

Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile
950 955 960

Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser
965 970 975

His Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly
980 985 990

Gln Arg Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys
995 1000 1005

Glu Asn Asn Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys
1010 1015 1020

Ile Cys Pro Pro Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile
1025 1030 1035

Asp His Cys Val Pro Glu Leu Asn Leu Cys Gln His Glu Ala Lys
1040 1045 1050

Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly
1055 1060 1065

Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala
1070 1075 1080

His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly
1085 1090 1095

Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu
1100 1105 1110

His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln
1115 1120 1125

Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu

1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu		
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu		
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln		
1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335
Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser		
1340	1345	1350

Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp
1355 1360 1365

Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly
1370 1375 1380

Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
1385 1390 1395

Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn
1400 1405 1410

Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
1415 1420 1425

Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly
1430 1435 1440

Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg
1445 1450 1455

Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala
1460 1465 1470

Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln
1475 1480 1485

Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
1490 1495 1500

Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu
1505 1510 1515

Glu Cys Gly Cys Leu Ala Cys Ser
1520

<210> 199

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 199

atggagattc ctgccaactt gccg 24

<210> 200

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 200

ttgttggcat tgaggaggag cagc 24

<210> 201

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 201

gagggcacg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202

<211> 753

<212> DNA

<213> Homo sapiens

<400> 202

ggatgcagga cgctcccctg agctgcctgt caccgactag gtggagcagt 50

gtttctccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100

gaatctgcct tttagttct gtctccggca ggctttgagg atgaaggctg 150

cgggcattct gacctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200

atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250

caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300

agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350

gactatggca tcttcagat caacagcttc gcgtggtgca gacgcggaaa 400

gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450

atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500

caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550

cctgtccgag tggaaaaaag gctgtgaggt ttctaaact ggaactggac 600

ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650

cctgtgtcat cttgtcccgt ttctcccaa tttccttct caaacttgga 700

gagggaaaat taagctatac tttaagaaa ataaatattt ccatttaa 750

gtc 753

<210> 203

<211> 148

<212> PRT

<213> Homo sapiens

<400> 203

Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr

1 5 10 15

Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile

20 25 30

Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly

35 40 45

Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr

50 55 60

Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe

65 70 75

Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu

80 85 90

Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
95 100 105

Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
110 115 120

Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
125 130 135

Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
140 145

<210> 204

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 204

gcaggctttg aggatgaagg ctgc 24

<210> 205

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 205

ctcattggct gcctggcac aggc 24

<210> 206

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 206

ccagtcggac aggtctctcc cctc 24

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

tcagtgacca aggctgagca ggcg 24

<210> 208

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 208

ctacactcgt tgcaactgg caaaaatatt ctgagggct ggcctgg 47

<210> 209

<211> 1648

<212> DNA

<213> Homo sapiens

<400> 209

caggccattt gcatccact gtccttgtgt tcggagccag gccacaccgt 50

cctcagcagt gtcattgttt aaaaacgcca agctgaatat atcatgcccc 100

tattaaaact tgtacatggc tccccattgg ttttggaga aaagttcaag 150

ctttttacct tgggtgtcgc ctgtatccca gtgttcaggc tggetagacg 200

gcggaagaag atcctatatt actgtcactt cccagatctg cttctacca 250

agagagattc ttttctaaa cgactataca gggccccaat tgactggata 300

gaggaatata ccacaggcat ggcagactgc atcttagtca acagccagtt 350

cacagctgct gttttaagg aaacattcaa gtcctgtct cacatagacc 400
ctgatgtcct ctatccatct ctaaagtca ccagcttga ctcagttgtt 450
cctgaaaage tggatgacct agtccccaag gggaaaaaat tcctgctgct 500
ctccatcaac agatacgaag ggaagaaaaa tctgactttg gcactggaag 550
ccctagtaca gctgctgga agattgacat cccaagattg ggagagggtt 600
catctgatcg tggcaggtgg ttatgacgag agagtcctgg agaattgga 650
acattatcag gaattgaaga aaatggtcca acagtccgac ctggccagt 700
atgtgacctt ctgaggtct ttctcagaca aacagaaaat ctccctctc 750
cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800
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cgggtggacc ctggagtc attgaccaca gtgtcacagg gttctgtgt 900
gagcctgacc cgggtgcatt ctcaagaagc atagaaaagt tcatccgtga 950
accttctta aaagccacca tgggcctggc tggaagagcc agagtgaagg 1000
aaaaatttc cctgaagca ttacagaac agctctaccg atatgttacc 1050
aaactgctgg tataatcaga ttgttttaa gatctccatt aatgtcatt 1100
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atgcagaaga gatcttttaaaaataaaact tgagtcctga atgtgagcca 1200
cttctctata taccacacct cctgtccac tttcagaaa aacctgtct 1250
tttatgctat aatcattcca aattttgcca gtgttaagtt acaaatgtgg 1300
tgtcattcca tgttcagcag agtattttaa ttatatctc tcgggattat 1350
tgctctctg tctataaatt ttgaatgata ctgtgcctta attggtttc 1400
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ataatgagag cagggctatt gtagttccca gattcaatcc accgaagtgt 1500

tcactgtcat ctgttaggga attttgttt gtctgtctt tgcctggatc 1550

catagcgaga gtgctctgta tttttttaa gataatttgt attttgcac 1600

actgagatat aataaaaggt gttatcata aaaaaaaaaa aaaaaaaaa 1648

<210> 210

<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly
1 5 10 15

Glu Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val
20 25 30

Phe Arg Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His
35 40 45

Phe Pro Asp Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg
50 55 60

Leu Tyr Arg Ala Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly
65 70 75

Met Ala Asp Cys Ile Leu Val Asn Ser Gln Phe Thr Ala Ala Val
80 85 90

Phe Lys Glu Thr Phe Lys Ser Leu Ser His Ile Asp Pro Asp Val
95 100 105

Leu Tyr Pro Ser Leu Asn Val Thr Ser Phe Asp Ser Val Val Pro
110 115 120

Glu Lys Leu Asp Asp Leu Val Pro Lys Gly Lys Lys Phe Leu Leu
125 130 135

Leu Ser Ile Asn Arg Tyr Glu Arg Lys Lys Asn Leu Thr Leu Ala
140 145 150

Leu Glu Ala Leu Val Gln Leu Arg Gly Arg Leu Thr Ser Gln Asp
155 160 165

Trp Glu Arg Val His Leu Ile Val Ala Gly Gly Tyr Asp Glu Arg
170 175 180

Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys Lys Met Val
185 190 195

Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg Ser Phe
200 205 210

Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys Val
215 220 225

Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu
230 235 240

Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly
245 250 255

Pro Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu
260 265 270

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg
275 280 285

Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg
290 295 300

Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr
305 310 315

Arg Tyr Val Thr Lys Leu Leu Val
320

<210> 211

<211> 1554

<212> DNA

<213> Homo sapiens

<400> 211

gactacgccg atccgagacg tggctccctg ggcggcagaa ccatgttgga 50

cttcgcgatc ttgccgtta ccttcttget ggcgttggtg ggagccgtgc 100
tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150
ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtgaag 200
tttgcattgag ttcttggtta attgcatga gagatatggg cctgtggtct 250
ccttctgggt ttgcaggcgc ctcgttggtta gtttgggcac tgttgatga 300
ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaacct 350
gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtga 400
accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttcttgaag 450
agtaactttg cctctcctct aaagctttca gaagaattat tagataaatg 500
gctctcctac ccagagacc agcacgtgcc cctcagccag catatgcttg 550
gttttgctat gaagtctgtt acacagatgg taatgggtag tacatttga 600
gatgatcagg aagtcattcg ctccagaag aatcatggca cagtttggtc 650
tgagattgga aaaggcttc tagatgggtc acttgataaa aacatgactc 700
ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgtttaagg 750
aacatcataa aagaacgaaa aggaaggaaac ttcagtcaac atatttcat 800
tgactcctta gtacaaggga acctaatga ccaacagatc ctagaagaca 850
gtatgatatt ttcttggcc agttgcataa taactgcaa attgtgtacc 900
tgggcaatct gtttttaac cacctctgaa gaagttcaaa aaaaattata 950
tgaagagata aaccaagttt ttggaatgg tcctgttact ccagagaaaa 1000
ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050
gccaaactga ctccagttc tgcccagctt caagatattg aaggaaaaat 1100
tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150

tggtacttca ggatcctaact acttggccat ctccacacaa gtttgatcca 1200

gatcggttg atgatgaatt agtaatgaaa acttttcct cacttggatt 1250

ctcaggcaca caggagtgtc cagagttgag gtttgcata atggtgacca 1300

cagtacttct tagtgattg gtgaagagac tgcacctact ttctgtggag 1350

ggacaggtta ttgaacaaa gtatgaactg gtaacatcat caaggaaga 1400

agcttgatc actgtctcaa agatatatta aaattttata catttaaat 1450

cattgtaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgtt 1500

aatccttta taaaccagta tcactttgta atataaacac ctattgtac 1550

ttaa 1554

<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu

1 5 10 15

Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala

20 25 30

Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu

35 40 45

Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn

50 55 60

Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg

65 70 75

Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His

80 85 90

Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys

95	100	105
Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn		
110	115	120
His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu		
125	130	135
Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu		
140	145	150
Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln His Val Pro Leu Ser		
155	160	165
Gln His Met Leu Gly Phe Ala Met Lys Ser Val Thr Gln Met Val		
170	175	180
Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile Arg Phe Gln		
185	190	195
Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly Phe Leu		
200	205	210
Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr Glu		
215	220	225
Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys		
230	235	240
Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser		
245	250	255
Leu Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser		
260	265	270
Met Ile Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys		
275	280	285
Thr Trp Ala Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys		
290	295	300
Lys Leu Tyr Glu Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val		
305	310	315

Thr Pro Glu Lys Ile Glu Gln Leu Arg Tyr Cys Gln His Val Leu
320 325 330

Cys Glu Thr Val Arg Thr Ala Lys Leu Thr Pro Val Ser Ala Gln
335 340 345

Leu Gln Asp Ile Glu Gly Lys Ile Asp Arg Phe Ile Ile Pro Arg
350 355 360

Glu Thr Leu Val Leu Tyr Ala Leu Gly Val Val Leu Gln Asp Pro
365 370 375

Asn Thr Trp Pro Ser Pro His Lys Phe Asp Pro Asp Arg Phe Asp
380 385 390

Asp Glu Leu Val Met Lys Thr Phe Ser Ser Leu Gly Phe Ser Gly
395 400 405

Thr Gln Glu Cys Pro Glu Leu Arg Phe Ala Tyr Met Val Thr Thr
410 415 420

Val Leu Leu Ser Val Leu Val Lys Arg Leu His Leu Leu Ser Val
425 430 435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
455 460

<210> 213

<211> 759

<212> DNA

<213> Homo sapiens

<400> 213

ctagatttgt cggcttgccg ggagacttca ggagtcgctg tctctgaact 50

tccagcctca gagaccgccg ccctgtccc cgagggccat gggccgggtc 100

tcagggttg tgcctctcg ctctctgacg ctctggcgc atctggtggt 150

cgatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200

ctctcacgtt cacccccgag gagtatgaca agcaggacat tcagctggtg 250

gccgcgtct ctgtcacctt gggcctctt gcagtggagc tggccggtt 300

cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350

gggctcactg tagtgcaccc gtggccctgt ccttcttcat attcagagcg 400

tgggagtga ctacgtattg gtacatttt gtcttctga gtgcccttc 450

agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500

aaccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550

ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600

ttccccctcg aaactgcttc tgctggagga tatgtgttg aataattacg 650

tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700

tgttttgtag taacattaag acttatatac agttttaggg gacaattaa 750

aaaaaaaa 759

<210> 214

<211> 140

<212> PRT

<213> Homo sapiens

<400> 214

Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu

1 5 10 15

Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp

20 25 30

Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu

35 40 45

Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr

50 55 60

Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val

65	70	75
Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His		
80	85	90
Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp		
95	100	105
Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu		
110	115	120
Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu		
125	130	135
Lys Lys Lys Pro Phe		
140		

<210> 215

<211> 697

<212> DNA

<213> Homo sapiens

<400> 215

tcccggaccc tgccgccctg ccactatgtc ccgccgtct atgtgcttg 50

cctgggtct cccagcctc ctgcactcg gagcggctca ggagacagaa 100

gacccggcct gctgcagccc catagtgtcc cggaacgagt ggaaggccct 150

ggcatcagag tgcgccagc acctgagcct gcccttacgc tatgtggtgg 200

tatgcacac ggcgggcagc agctgcaaca ccccgctc gtgccagcag 250

caggcccga atgtgcagca ctaccatg aagacactgg gctggtgcga 300

cgtgggtac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350

gtggctgga cttcacgggt gccactcag gtcactatg gaacccatg 400

tccattggca tcagttcat gggcaactac atggatcggg tgccacacc 450

ccaggccatc cgggcagccc agggcttact ggcctgcggt gtggctcagg 500

gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550

acactctctc caggcaacca gctctaccac ctcattccaga attggccaca 600

ctaccgtcc ccctgaggcc ctgctgatcc gcacccatt cctcccctcc 650

catggccaaa aaccccactg tctccttctc caataaagat gtagctc 697

<210> 216

<211> 196

<212> PRT

<213> Homo sapiens

<400> 216

Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu

1 5 10 15

Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys

20 25 30

Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu

35 40 45

Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser

50 55 60

His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln

65 70 75

Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp

80 85 90

Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val

95 100 105

Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His

110 115 120

Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr

125 130 135

Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly

140 145 150

Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr
155 160 165

Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly
170 175 180

Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser
185 190 195

Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

ctgggacccc gaaaagagaa ggggagagcg aggggacgag agcggaggag 50

gaagatgcaa ctgactcgct gctgcttcgt gttcctggcg cagggtagcc 100

tctatctggt catctgtggc caggatgatg gtcctcccgg ctcagaggac 150

cctgagcgtg atgaccacga gggccagccc cggccccggg tgcctcggaa 200

gcgggggccac atctcaccta agtcccggcc catggccaat tccactctcc 250

tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc 300

cccaaccgcc cgaaccacag cccccaccc tcagccaagg tgaagaaaat 350

ctttggctgg ggcgacttct actccaacat caagacggcg gccctgaacc 400

tgctcgtcac agggaagatt gtggaccatg gcaatgggac cttcagcgtc 450

cacttccaac acaatgccac aggccaggga aacatctcca tcagcctcgt 500

gccccccagt aaagtgtag agttccacca ggaacagcag atcttcatcg 550

aagccaaggc ctccaaaatc ttaactgcc ggatggagtg ggagaaggta 600

gaacggggcc gccggacctc gctttgcacc cagacccag ccaagatctg 650

ctcccagac cacgctcaga gctcagccac ctggagctgc tcccagccct 700
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gtccagaagg tgtgcccaga ttacaactac catagtata cccctacta 800
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gcagcgggca cgggtggggc ggggccgggc cgagagcat gtgtggatc 1750

tggtctgtgt gtctgtctgt ggggtgggggg aggggaggga agtcttgtga 1800

aaccgctgat tgcgtacttt tgtgtgaaga atcgtgttct tggagcagga 1850

aataaagctt gccccggggc a 1871

<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

Met Gln Leu Thr Arg Cys Cys Phe Val Phe Leu Val Gln Gly Ser

1 5 10 15

Leu Tyr Leu Val Ile Cys Gly Gln Asp Asp Gly Pro Pro Gly Ser

20 25 30

Glu Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg

35 40 45

Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met

50 55 60

Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala

65 70 75

Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro

80 85 90

Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe

95 100 105

Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly

110 115 120

Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln

125 130 135

His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro

140 145 150

Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile

155	160	165
Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu		
170	175	180
Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro		
185	190	195
Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp		
200	205	210
Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe		
215	220	225
Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr		
230	235	240
Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly		
245	250	

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150

agctcgaggg gagactttga ctcaagcca cagaattggt ggaagtgtgc 200

gcgccgccgc cgccgtcgct cctgcagcgc tgtcgaccta gccgctagca 250

tcttcccgag caccgggatc ccggggtagg aggcgacgcg ggcgagcacc 300

agcggcagcc ggctgcggct gcccacacgg ctcacatgg gctccgggcg 350

ccggggcgctg tccgcggtgc cgccgtgct gctggtcctc acgctgccgg 400

ggctgcccgt ctgggcacag aacgacacgg agcccatcgt gctggagggc 450

aagtgtctgg tgggtgcga ctcgaacccg gccacggact ccaagggctc 500
ctcttctcc ccgctgggga tatcgggccg ggcggccaac tccaaggtcg 550
ccttctcggc ggtgcggagc accaaccacg agccatccga gatgagcaac 600
aagacgcgca tcatttactt cgtacagatc ctggtgaatg tgggtaattt 650
ttcacattg gagtctgtct ttgtagcacc aagaaaagga atttacagtt 700
tcagttttca cgtgattaaa gtctaccaga gccaaactat ccaggttaac 750
ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaaga 800
tgttactcgt gaagctgcc acaatggtgt cctgctctac ctagataaag 850
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tttccatga tgttcatcca ggtgagggat gaccactcc tgagttattg 1000
gaagatcatt ttttcatcat tggattgatg tcttttattg gtttctcatg 1050
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gaatgctca tagtgtatt ttaattgtat atgtgaaaga gtcataat 1600

ccaagtata ttttctaaga agaagaatag atcataaatc tgacaaggaa 1650

aaagttgctt acccaaaatc taagtgtca atccctgagc ctcagcaaaa 1700

cagctccctt ccgagggaat tcttatactt tattgtctca cttaattaa 1750

aatgattgat aataaccact ttataaaaa cctaagggtt ttttttttc 1800

cgtagacatg accactttat taactgggtg tgggatgctg ttgtttctaa 1850

ttatacctat ttttcaagge ttctgttgta ttgaagtat catctgggtt 1900

tgccttaact ctttaaattg tatatattta tctgtttagc taatattaaa 1950

ttcaaatatc ccatacttaa atttagtgca atatctgtc tttgtatag 2000

gtcatatgaa ttcataaaat tatttatgtc tgttatagaa taaagattaa 2050

tatatgttaa aaaaa 2065

<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

Met Gly Ser Gly Arg Arg Ala Leu Ser Ala Val Pro Ala Val Leu

1 5 10 15

Leu Val Leu Thr Leu Pro Gly Leu Pro Val Trp Ala Gln Asn Asp

20 25 30

Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp

35 40 45

Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu

50 55 60

Gly Ile Ser Val Arg Ala Ala Asn Ser Lys Val Ala Phe Ser Ala

65 70 75

Val Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Lys Thr
80 85 90

Arg Ile Ile Tyr Phe Asp Gln Ile Leu Val Asn Val Gly Asn Phe
95 100 105

Phe Thr Leu Glu Ser Val Phe Val Ala Pro Arg Lys Gly Ile Tyr
110 115 120

Ser Phe Ser Phe His Val Ile Lys Val Tyr Gln Ser Gln Thr Ile
125 130 135

Gln Val Asn Leu Met Leu Asn Gly Lys Pro Val Ile Ser Ala Phe
140 145 150

Ala Gly Asp Lys Asp Val Thr Arg Glu Ala Ala Thr Asn Gly Val
155 160 165

Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu
170 175 180

Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly
185 190 195

Phe Leu Val Phe Pro Leu
200

<210> 221

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 221

acggctcacc atgggctccg 20

<210> 222

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 222

aggaagagga gcccttgag tccg 24

<210> 223

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 223

cgtgctggag ggcaagtgc tgggtgtg cgactgaac 40

<210> 224

<211> 902

<212> DNA

<213> Homo sapiens

<400> 224

cgggtggcat gactcggcc gtgttctcg gctgcgctt cattgccttc 50

gggcctgcgc tcgccctta tgtctcacc atgccatcg agccgttgcg 100

tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150

tttcgtccct tgtttggtc atggcaagag tcattattga caacaaagat 200

ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250

tatccaagaa atgttccgat ttgcatatta taaactctta aaaaaagcca 300

gtgaaggttt gaagagtata aaccaggtg agacagcacc ctctatgcga 350

ctgctggcct atgtttctgg ctgggcttt ggaatcatga gtggagtatt 400

ttcctttgtg aataccctat ctgactcctt ggggccaggc acagtgggca 450

ttcatggaga ttctcctcaa ttcttccttt attcagcttt catgacgctg 500

gtcattatct tgctgcatgt attctggggc attgtatttt ttgatggctg 550

tgagaagaaa aagtggggca tcctccttat cgttcctctg acccacctgc 600

tggtgtcagc ccagaccttc ataagttcctt attatggaat aaacctggcg 650

tcagcattta taatcctggg gctcatgggc acctgggcat tcttagctgc 700

gggaggcagc tgccgaagcc tgaaactctg cctgctctgc caagacaaga 750

actttcttct ttacaaccag cgctccagat aacctcaggg aaccagcact 800

tcccaaaccg cagactacat ctttagagga agcacaactg tgccttttc 850

tgaaaatccc ttttctggg ggaattgaga aagaaataaa actatgcaga 900

ta 902

<210> 225

<211> 257

<212> PRT

<213> Homo sapiens

<400> 225

Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly

1 5 10 15

Pro Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Ile Glu Pro Leu

20 25 30

Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser

35 40 45

Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile

50 55 60

Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly

65 70 75

Ala Phe Val Ser Val Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr

80 85 90

Tyr Lys Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn

95	100	105
Pro Gly Glu Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser		
110	115	120
Gly Leu Gly Phe Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn		
125	130	135
Thr Leu Ser Asp Ser Leu Gly Pro Gly Thr Val Gly Ile His Gly		
140	145	150
Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala Phe Met Thr Leu Val		
155	160	165
Ile Ile Leu Leu His Val Phe Trp Gly Ile Val Phe Phe Asp Gly		
170	175	180
Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val Leu Leu Thr		
185	190	195
His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr Tyr Gly		
200	205	210
Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly Thr		
215	220	225
Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu		
230	235	240
Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr Asn Gln Arg		
245	250	255

Ser Arg

<210> 226

<211> 3939

<212> DNA

<213> Homo sapiens

<400> 226

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atgttcgctc tgggcttgcc ctcttggtg ctcttggtg cctcggcga 100
gagccatctg ggggttctgg ggccaagaa cgtctgcag aaagacgccg 150
agtttgagcg cacctacgtg gacgaggtca acagcgagct ggtcaacatc 200
tacacctca accatactgt gacccgcaac aggacagagg gcgtgcgtgt 250
gtctgtgaac gtcctgaaca agcagaaggg ggcgccgtg ctgtttgtgg 300
tccgccagaa ggaggctgtg gtgtccttc aggtgccct aatcctgcga 350
gggatgttc agcgcaagta cctctacaa aaagtggaac gaacctgtg 400
tcagcccc accaagaatg agtcggagat tcagttctc tacgtggatg 450
tgtccacct gtcaccagtc aacaccacat accagctccg ggtcagccgc 500
atggacgatt ttgtgctcag gactggggag cagttcagct tcaataccac 550
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<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

Met Phe Ala Leu Gly Leu Pro Phe Leu Val Leu Leu Val Ala Ser

1 5 10 15

Val Glu Ser His Leu Gly Val Leu Gly Pro Lys Asn Val Ser Gln

20 25 30

Lys Asp Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu Val Asn Ser

35 40 45

Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn

50 55 60

Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys Gln

65	70	75
Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val		
80	85	90
Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg		
95	100	105
Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro		
110	115	120
Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser		
125	130	135
Thr Leu Ser Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg		
140	145	150
Met Asp Asp Phe Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn		
155	160	165
Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu		
170	175	180
Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn Lys Ala Phe		
185	190	195
Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro Val Tyr		
200	205	210
Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr Met		
215	220	225
Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser		
230	235	240
Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala		
245	250	255
Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro		
260	265	270
Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser		
275	280	285

Gln Ala Val Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys
290 295 300

Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala
305 310 315

Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala
320 325 330

Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala
335 340 345

Asp Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly
350 355 360

Ser Phe Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser
365 370 375

Ala Gly Thr Gly Asp Leu Ser Tyr Gly Tyr Gln Gly Arg Ser Phe
380 385 390

Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val
395 400 405

Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys
410 415 420

Asn Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala
425 430 435

Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe
440 445 450

Trp Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val
455 460 465

Gln Leu Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn
470 475 480

Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly
485 490 495

Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile

500	505	510
Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile		
515	520	525
Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu Glu		
530	535	540
Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr		
545	550	555
Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys		
560	565	570
Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met		
575	580	585
Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro		
590	595	600
Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile		
605	610	615
Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn		
620	625	630
Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr		
635	640	645
Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu		
650	655	660
Asp Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp		
665	670	675
Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val		
680	685	690
Leu Leu Val Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr		
695	700	705
Gly Leu Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala		
710	715	720

Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile
725 730 735

Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu
740 745 750

Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu Phe Phe
755 760 765

Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu Ser
770 775 780

Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp
785 790 795

His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser
800 805 810

Phe Leu Val Leu Leu Thr Leu Asp Asp Asp Leu Asp Thr Val Gln
815 820 825

Arg Asp Lys Ile Tyr Val Phe
830

<210> 228

<211> 2848

<212> DNA

<213> Homo sapiens

<400> 228

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ttgggcgctg gagggcctgt cctgaccatg gtcctgcct ggctgtggct 150

gctttgtgtc tccgtccccc aggctctccc caaggcccag cctgcagagc 200

tgtctgtgga agttccagaa aactatggtg gaaatttccc ttatacctg 250

accaagttgc cgctgccccg tgagggggct gaaggccaga tcgtgctgtc 300

aggggactca ggcaaggcaa ctgaggggccc atttgctatg gatccagatt 350

ctggcttct gctggtgacc agggccctgg accgagagga gcaggcagag 400
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<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

Met Val Pro Ala Trp Leu Trp Leu Leu Cys Val Ser Val Pro Gln
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Ala Leu Pro Lys Ala Gln Pro Ala Glu Leu Ser Val Glu Val Pro
 20 25 30

Glu Asn Tyr Gly Gly Asn Phe Pro Leu Tyr Leu Thr Lys Leu Pro
 35 40 45

Leu Pro Arg Glu Gly Ala Glu Gly Gln Ile Val Leu Ser Gly Asp
 50 55 60

Ser Gly Lys Ala Thr Glu Gly Pro Phe Ala Met Asp Pro Asp Ser
 65 70 75

Gly Phe Leu Leu Val Thr Arg Ala Leu Asp Arg Glu Glu Gln Ala
 80 85 90

Glu Tyr Gln Leu Gln Val Thr Leu Glu Met Gln Asp Gly His Val
 95 100 105

Leu Trp Gly Pro Gln Pro Val Leu Val His Val Lys Asp Glu Asn
 110 115 120

Asp Gln Val Pro His Phe Ser Gln Ala Ile Tyr Arg Ala Arg Leu

125	130	135
Ser Arg Gly Thr Arg Pro Gly Ile Pro Phe Leu Phe Leu Glu Ala		
140	145	150
Ser Asp Arg Asp Glu Pro Gly Thr Ala Asn Ser Asp Leu Arg Phe		
155	160	165
His Ile Leu Ser Gln Ala Pro Ala Gln Pro Ser Pro Asp Met Phe		
170	175	180
Gln Leu Glu Pro Arg Leu Gly Ala Leu Ala Leu Ser Pro Lys Gly		
185	190	195
Ser Thr Ser Leu Asp His Ala Leu Glu Arg Thr Tyr Gln Leu Leu		
200	205	210
Val Gln Val Lys Asp Met Gly Asp Gln Ala Ser Gly His Gln Ala		
215	220	225
Thr Ala Thr Val Glu Val Ser Ile Ile Glu Ser Thr Trp Val Ser		
230	235	240
Leu Glu Pro Ile His Leu Ala Glu Asn Leu Lys Val Leu Tyr Pro		
245	250	255
His His Met Ala Gln Val His Trp Ser Gly Gly Asp Val His Tyr		
260	265	270
His Leu Glu Ser His Pro Pro Gly Pro Phe Glu Val Asn Ala Glu		
275	280	285
Gly Asn Leu Tyr Val Thr Arg Glu Leu Asp Arg Glu Ala Gln Ala		
290	295	300
Glu Tyr Leu Leu Gln Val Arg Ala Gln Asn Ser His Gly Glu Asp		
305	310	315
Tyr Ala Ala Pro Leu Glu Leu His Val Leu Val Met Asp Glu Asn		
320	325	330
Asp Asn Val Pro Ile Cys Pro Pro Arg Asp Pro Thr Val Ser Ile		
335	340	345

Pro Glu Leu Ser Pro Pro Gly Thr Glu Val Thr Arg Leu Ser Ala
350 355 360

Glu Asp Ala Asp Ala Pro Gly Ser Pro Asn Ser His Val Val Tyr
365 370 375

Gln Leu Leu Ser Pro Glu Pro Glu Asp Gly Val Glu Gly Arg Ala
380 385 390

Phe Gln Val Asp Pro Thr Ser Gly Ser Val Thr Leu Gly Val Leu
395 400 405

Pro Leu Arg Ala Gly Gln Asn Ile Leu Leu Leu Val Leu Ala Met
410 415 420

Asp Leu Ala Gly Ala Glu Gly Gly Phe Ser Ser Thr Cys Glu Val
425 430 435

Glu Val Ala Val Thr Asp Ile Asn Asp His Ala Pro Glu Phe Ile
440 445 450

Thr Ser Gln Ile Gly Pro Ile Ser Leu Pro Glu Asp Val Glu Pro
455 460 465

Gly Thr Leu Val Ala Met Leu Thr Ala Ile Asp Ala Asp Leu Glu
470 475 480

Pro Ala Phe Arg Leu Met Asp Phe Ala Ile Glu Arg Gly Asp Thr
485 490 495

Glu Gly Thr Phe Gly Leu Asp Trp Glu Pro Asp Ser Gly His Val
500 505 510

Arg Leu Arg Leu Cys Lys Asn Leu Ser Tyr Glu Ala Ala Pro Ser
515 520 525

His Glu Val Val Val Val Val Gln Ser Val Ala Lys Leu Val Gly
530 535 540

Pro Gly Pro Gly Pro Gly Ala Thr Ala Thr Val Thr Val Leu Val
545 550 555

Glu Arg Val Met Pro Pro Pro Lys Leu Asp Gln Glu Ser Tyr Glu

560	565	570
Ala Ser Val Pro Ile Ser Ala Pro Ala Gly Ser Phe Leu Leu Thr		
575	580	585
Ile Gln Pro Ser Asp Pro Ile Ser Arg Thr Leu Arg Phe Ser Leu		
590	595	600
Val Asn Asp Ser Glu Gly Trp Leu Cys Ile Glu Lys Phe Ser Gly		
605	610	615
Glu Val His Thr Ala Gln Ser Leu Gln Gly Ala Gln Pro Gly Asp		
620	625	630
Thr Tyr Thr Val Leu Val Glu Ala Gln Asp Thr Ala Leu Thr Leu		
635	640	645
Ala Pro Val Pro Ser Gln Tyr Leu Cys Thr Pro Arg Gln Asp His		
650	655	660
Gly Leu Ile Val Ser Gly Pro Ser Lys Asp Pro Asp Leu Ala Ser		
665	670	675
Gly His Gly Pro Tyr Ser Phe Thr Leu Gly Pro Asn Pro Thr Val		
680	685	690
Gln Arg Asp Trp Arg Leu Gln Thr Leu Asn Gly Ser His Ala Tyr		
695	700	705
Leu Thr Leu Ala Leu His Trp Val Glu Pro Arg Glu His Ile Ile		
710	715	720
Pro Val Val Val Ser His Asn Ala Gln Met Trp Gln Leu Leu Val		
725	730	735
Arg Val Ile Val Cys Arg Cys Asn Val Glu Gly Gln Cys Met Arg		
740	745	750
Lys Val Gly Arg Met Lys Gly Met Pro Thr Lys Leu Ser Ala Val		
755	760	765
Gly Ile Leu Val Gly Thr Leu Val Ala Ile Gly Ile Phe Leu Ile		
770	775	780

Leu Ile Phe Thr His Trp Thr Met Ser Arg Lys Lys Asp Pro Asp
785 790 795

Gln Pro Ala Asp Ser Val Pro Leu Lys Ala Thr Val
800 805

<210> 230

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 230

cgccttaccg cgcagcccga agattcacta tggtgaaaat cgccttcaat 50

<210> 231

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 231

cctgagctgt aacccactc cagg 24

<210> 232

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

agagtctgtc ccagctatct tgt 23

<210> 233

<211> 2786

<212> DNA

<213> Homo sapiens

<400> 233

ccggggacat gaggtggata ctgttcattg gggcccttat tgggtccagc 50
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cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150
acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200
gatgtcctgg tcccatctgt cagtctgcag gcatttaaat ccttcctgag 250
atcccagggc ttagagtacg cagtgacaat tgaggacctg caggcccttt 300
tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350
agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400
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<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

Met Arg Trp Ile Leu Phe Ile Gly Ala Leu Ile Gly Ser Ser Ile

1 5 10 15

Cys Gly Gln Glu Lys Phe Phe Gly Asp Gln Val Leu Arg Ile Asn

20 25 30

Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn

35 40 45

Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe

50 55 60

Asn Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala
65 70 75

Phe Lys Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr
80 85 90

Ile Glu Asp Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met
95 100 105

Gln His Asn Glu Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr
110 115 120

Gly Ala Tyr His Ser Leu Glu Ala Ile Tyr His Glu Met Asp Asn
125 130 135

Ile Ala Ala Asp Phe Pro Asp Leu Ala Arg Arg Val Lys Ile Gly
140 145 150

His Ser Phe Glu Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr
155 160 165

Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu Asn Ala Gly Ile
170 175 180

His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile Trp Thr Ala
185 190 195

Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp Pro Ala Ile Thr Ser
200 205 210

Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro Val Ala Asn Pro
215 220 225

Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys
230 235 240

Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro
245 250 255

Asn Arg Asn Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp
260 265 270

Asn Pro Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu

275	280	285
Val Glu Val Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn		
290	295	300
Phe Lys Gly Phe Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met		
305	310	315
Tyr Pro Tyr Gly Tyr Ser Val Lys Lys Ala Pro Asp Ala Glu Glu		
320	325	330
Leu Asp Lys Val Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser Val		
335	340	345
Ser Gly Thr Glu Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Tyr		
350	355	360
Pro Ala Ser Gly Ser Ser Ile Asp Trp Ala Tyr Asp Asn Gly Ile		
365	370	375
Lys Phe Ala Phe Thr Phe Glu Leu Arg Asp Thr Gly Thr Tyr Gly		
380	385	390
Phe Leu Leu Pro Ala Asn Gln Ile Ile Pro Thr Ala Glu Glu Thr		
395	400	405
Trp Leu Gly Leu Lys Thr Ile Met Glu His Val Arg Asp Asn Leu		
410	415	420

Tyr

<210> 235

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 235

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ctgtgctcca atctactgtg tgtccccggc caatgcccc agtgcatacc 150

ccgcccctc ctecacaaag agcaccctg cctcacaggt gtattccctc 200
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236

<211> 417

<212> PRT

<213> Homo sapiens

<400> 236

Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val Gly Leu Cys

1 5 10 15

Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr

20 25 30

Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr

35 40 45

Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val

50 55 60

Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val

65 70 75

Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr

80 85 90

Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr
95 100 105

Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser
110 115 120

Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala
125 130 135

Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly
140 145 150

Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe
155 160 165

Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys
170 175 180

Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp
185 190 195

Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala
200 205 210

Lys Trp Glu Lys Pro Phe His Leu Glu Tyr Thr Arg Lys Asn Phe
215 220 225

Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln Val Pro Met Met
230 235 240

His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn
245 250 255

Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe
260 265 270

Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala
275 280 285

Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys
290 295 300

Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser

305	310	315
Tyr Asn Leu Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala		
320	325	330
Phe Asp Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser		
335	340	345
Leu Gln Val Ser Lys Ala Thr His Lys Ala Val Leu Asp Val Ser		
350	355	360
Glu Glu Gly Thr Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile		
365	370	375
Val Arg Ser Lys Asp Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn		
380	385	390
Arg Thr Phe Leu Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile		
395	400	405
Leu Phe Leu Gly Lys Val Glu Asn Pro Thr Lys Ser		
410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

cttgctgtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 239

tgactcgggg tctccaaac cagc 24

<210> 240

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 240

ggtataggcg gaaggcaaag tcgg 24

<210> 241

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 241

ggcatcttac cttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242

<211> 2436

<212> DNA

<213> Homo sapiens

<400> 242

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gatgaactca gttataggag aaaacctcca tgctggactc catctggcat 2350

tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaa aaaaaaaaaa 2400

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

Met Lys Met Gln Lys Gly Asn Val Leu Leu Met Phe Gly Leu Leu

1 5 10 15

Leu His Leu Glu Ala Ala Thr Asn Ser Asn Glu Thr Ser Thr Ser

20 25 30

Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala

35 40 45

Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala

50 55 60

Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val

65 70 75

Thr Asn Ser Glu Phe His Thr Thr Ser Ser Gly Ile Ser Thr Ala

80 85 90

Thr Asn Ser Glu Phe Ser Thr Ala Ser Ser Gly Ile Ser Ile Ala

95 100 105

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala

110 115 120

Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Ser Thr Val

125 130 135

Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Ala Ser Thr Ala

140 145 150

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
155 160 165

Thr Asn Ser Glu Ser Ser Thr Leu Ser Ser Gly Ala Ser Thr Ala
170 175 180

Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
185 190 195

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
200 205 210

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
215 220 225

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
230 235 240

Thr Asn Ser Glu Ser Arg Thr Thr Ser Asn Gly Ala Gly Thr Ala
245 250 255

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
260 265 270

Thr Asn Ser Asp Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala
275 280 285

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
290 295 300

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
305 310 315

Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Gly Thr Ala
320 325 330

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val
335 340 345

Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Asn Thr Ala
350 355 360

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala

365	370	375
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala		
380	385	390
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala		
395	400	405
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala		
410	415	420
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala		
425	430	435
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val		
440	445	450
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala		
455	460	465
Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala		
470	475	480
Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala		
485	490	495
Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile		
500	505	510
Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe		
515	520	525
Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn		
530	535	540
Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly		
545	550	555
Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro		
560	565	570
Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile		
575	580	585

Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro
590 595

<210> 244

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

ggaccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

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tcctctcttc tgctactggg ggcctgtct ggatgggcgg ccagcgatga 150
ccccattgag aaggtcattg aagggatcaa ccgagggtg agcaatgcag 200
agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250
gccggaaggg aagtggagaa ggttttaac ggacttagca acatggggag 300
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gaagcagaga agcttgcca tgggtcaac aacgtgctg gacaggccgg 450
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gttgtcacat cagctgacat gacctggagg ggttgggggt gggggacagg 900
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<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu Leu
1 5 10 15

Leu Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu
20 25 30

Lys Val Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg
35 40 45

Glu Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His
50 55 60

Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met
65 70 75

Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu
80 85 90

Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His Gly Ile
95 100 105

Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val Asn
110 115 120

Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln
125 130 135

Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys
140 145 150

Leu Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu
155 160 165

Val Glu Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala
170 175 180

Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser
185 190 195

Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser
200 205 210

Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly
215 220 225

Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
230 235 240

Ser Val Ala Asn Ile Met Pro
245

<210> 249

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 249

caatatgcat ctgcacgtc tgg 23

<210> 250

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 250

aagttctct gettccttc ctgc 24

<210> 251

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 251

tgacccatt gagaaggta ttgaaggat caaccgagg ctg 43

<210> 252

<211> 3781

<212> DNA

<213> Homo sapiens

<400> 252

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cagtggacac tccaggaaga gcggccccgc gggggggcgat gaccgtgcgc 100
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 gtctgaagaa ttactgtta aaaaaaaaa a 3781

<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp Leu Ala Ala Pro

1 5 10 15

Trp Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu Leu

20 25 30

Leu Leu Leu Leu Leu Gln Pro Pro Pro Pro Thr Trp Ala Leu Ser

35 40 45

Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu

50 55 60

Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu
65 70 75

Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu
80 85 90

Phe Ala Leu Ser Ser Asn Leu Ser Phe Leu Pro Gly Gly Glu Tyr
95 100 105

Gln Glu Leu Leu Trp Gly Ala Asp Ala Glu Lys Lys Gln Gln Cys
110 115 120

Ser Phe Lys Gly Lys Asp Pro Gln Arg Asp Cys Gln Asn Tyr Ile
125 130 135

Lys Ile Leu Leu Pro Leu Ser Gly Ser His Leu Phe Thr Cys Gly
140 145 150

Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr Ile Asn Met Glu Asn
155 160 165

Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val Leu Leu Glu Asp
170 175 180

Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys Ser Thr Ala
185 190 195

Leu Val Val Asp Gly Glu Leu Tyr Thr Gly Thr Val Ser Ser Phe
200 205 210

Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser Gln Ser Leu Arg Pro
215 220 225

Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe
230 235 240

Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly Ser Leu Gln Gly
245 250 255

Asp Asp Asp Lys Ile Tyr Phe Phe Phe Ser Glu Thr Gly Gln Glu
260 265 270

Phe Glu Phe Phe Glu Asn Thr Ile Val Ser Arg Ile Ala Arg Ile

275	280	285
Cys Lys Gly Asp Glu Gly Gly Glu Arg Val Leu Gln Gln Arg Trp		
290	295	300
Thr Ser Phe Leu Lys Ala Gln Leu Leu Cys Ser Arg Pro Asp Asp		
305	310	315
Gly Phe Pro Phe Asn Val Leu Gln Asp Val Phe Thr Leu Ser Pro		
320	325	330
Ser Pro Gln Asp Trp Arg Asp Thr Leu Phe Tyr Gly Val Phe Thr		
335	340	345
Ser Gln Trp His Arg Gly Thr Thr Glu Gly Ser Ala Val Cys Val		
350	355	360
Phe Thr Met Lys Asp Val Gln Arg Val Phe Ser Gly Leu Tyr Lys		
365	370	375
Glu Val Asn Arg Glu Thr Gln Gln Trp Tyr Thr Val Thr His Pro		
380	385	390
Val Pro Thr Pro Arg Pro Gly Ala Cys Ile Thr Asn Ser Ala Arg		
395	400	405
Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu		
410	415	420
Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln Val Arg Ser		
425	430	435
Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg Val Ala		
440	445	450
Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu Phe		
455	460	465
Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly		
470	475	480
Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly		
485	490	495

Gln Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu
500 505 510

Tyr Ala Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn
515 520 525

Cys Ser Leu Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp
530 535 540

Pro Tyr Cys Ala Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu
545 550 555

Tyr Gln Pro Gln Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu
560 565 570

Gly Ala Ser Ala Lys Asp Leu Cys Ser Ala Ser Ser Val Val Ser
575 580 585

Pro Ser Phe Val Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln
590 595 600

Phe Gln Pro Asn Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser
605 610 615

Asn Leu Ala Thr Arg Leu Trp Leu Arg Asn Gly Ala Pro Val Asn
620 625 630

Ala Ser Ala Ser Cys His Val Leu Pro Thr Gly Asp Leu Leu Leu
635 640 645

Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu
650 655 660

Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val
665 670 675

Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser Val Pro
680 685 690

Val Ile Ile Ser Thr Ser Arg Val Ser Ala Pro Ala Gly Gly Lys
695 700 705

Ala Ser Trp Gly Ala Asp Arg Ser Tyr Trp Lys Glu Phe Leu Val

710	715	720
Met Cys Thr Leu Phe Val Leu Ala Val Leu Leu Pro Val Leu Phe		
725	730	735
Leu Leu Tyr Arg His Arg Asn Ser Met Lys Val Phe Leu Lys Gln		
740	745	750
Gly Glu Cys Ala Ser Val His Pro Lys Thr Cys Pro Val Val Leu		
755	760	765
Pro Pro Glu Thr Arg Pro Leu Asn Gly Leu Gly Pro Pro Ser Thr		
770	775	780
Pro Leu Asp His Arg Gly Tyr Gln Ser Leu Ser Asp Ser Pro Pro		
785	790	795
Gly Ala Arg Val Phe Thr Glu Ser Glu Lys Arg Pro Leu Ser Ile		
800	805	810
Gln Asp Ser Phe Val Glu Val Ser Pro Val Cys Pro Arg Pro Arg		
815	820	825
Val Arg Leu Gly Ser Glu Ile Arg Asp Ser Val Val		
830	835	

<210> 254

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 254

agcccgtagca gaatctgctc ctgg 24

<210> 255

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 255

tgaagccagg gcagcgtcct ctgg 24

<210> 256

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 256

gtacaggctg cagttggc 18

<210> 257

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 257

agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 258

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<210> 259

<211> 4563

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 3635

<223> unknown base

<400> 259

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cgcgcgagcc gccgctagcg cgcgccgggc atggtccct cttaaaggcg 250

caggccgcgg cggcgggggc ggggtgtcgg aacaaagcgc cggcgcgggg 300

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gcggcgctgc ccgggccggg cctcgcggcg ctagggcggg ctggcctccg 400

tgggcggggg cagcgggctg agggcgcgcg gagcctgcgg cggcggcggc 450

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gcccacggcg ccgcgccagc ccgagggct gccggtccgg gcaggcggcg 650

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ccagtgaaca atatttttct attgtacttt tcgaaccatt ttgtctcatt 4500

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aaacacgaaa aaa 4563

<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

Met Ala Ala Arg Gly Arg Arg Ala Trp Leu Ser Val Leu Leu Gly

1 5 10 15

Leu Val Leu Gly Phe Val Leu Ala Ser Arg Leu Val Leu Pro Arg

20 25 30

Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro

35 40 45

Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly

50 55 60

Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser

65 70 75

Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly

80 85 90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala

95 100 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe

110 115 120

Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro
125 130 135

Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
140 145 150

Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu
155 160 165

Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg
170 175 180

Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe
185 190 195

Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu
200 205 210

Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val
215 220 225

Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
230 235 240

Lys Cys Leu Arg Glu Met Tyr Thr Thr His Glu Asp Val Glu Val
245 250 255

Gly Arg Cys Val Arg Arg Phe Ala Gly Val Gln Cys Val Trp Ser
260 265 270

Tyr Glu Met Arg Gln Leu Phe Tyr Glu Asn Tyr Glu Gln Asn Lys
275 280 285

Lys Gly Tyr Ile Arg Asp Leu His Asn Ser Lys Ile His Gln Ala
290 295 300

Ile Thr Leu His Pro Asn Lys Asn Pro Pro Tyr Gln Tyr Arg Leu
305 310 315

His Ser Tyr Met Leu Ser Arg Lys Ile Ser Glu Leu Arg His Arg
320 325 330

Thr Ile Gln Leu His Arg Glu Ile Val Leu Met Ser Lys Tyr Ser

335	340	345
Asn Thr Glu Ile His Lys Glu Asp Leu Gln Leu Gly Ile Pro Pro		
350	355	360
Ser Phe Met Arg Phe Gln Pro Arg Gln Arg Glu Glu Ile Leu Glu		
365	370	375
Trp Glu Phe Leu Thr Gly Lys Tyr Leu Tyr Ser Ala Val Asp Gly		
380	385	390
Gln Pro Pro Arg Arg Gly Met Asp Ser Ala Gln Arg Glu Ala Leu		
395	400	405
Asp Asp Ile Val Met Gln Val Met Glu Met Ile Asn Ala Asn Ala		
410	415	420
Lys Thr Arg Gly Arg Ile Ile Asp Phe Lys Glu Ile Gln Tyr Gly		
425	430	435
Tyr Arg Arg Val Asn Pro Met Tyr Gly Ala Glu Tyr Ile Leu Asp		
440	445	450
Leu Leu Leu Leu Tyr Lys Lys His Lys Gly Lys Lys Met Thr Val		
455	460	465
Pro Val Arg Arg His Ala Tyr Leu Gln Gln Thr Phe Ser Lys Ile		
470	475	480
Gln Phe Val Glu His Glu Glu Leu Asp Ala Gln Glu Leu Ala Lys		
485	490	495
Arg Ile Asn Gln Glu Ser Gly Ser Leu Ser Phe Leu Ser Asn Ser		
500	505	510
Leu Lys Lys Leu Val Pro Phe Gln Leu Pro Gly Ser Lys Ser Glu		
515	520	525
His Lys Glu Pro Lys Asp Lys Lys Ile Asn Ile Leu Ile Pro Leu		
530	535	540
Ser Gly Arg Phe Asp Met Phe Val Arg Phe Met Gly Asn Phe Glu		
545	550	555

Lys Thr Cys Leu Ile Pro Asn Gln Asn Val Lys Leu Val Val Leu
560 565 570

Leu Phe Asn Ser Asp Ser Asn Pro Asp Lys Ala Lys Gln Val Glu
575 580 585

Leu Met Arg Asp Tyr Arg Ile Lys Tyr Pro Lys Ala Asp Met Gln
590 595 600

Ile Leu Pro Val Ser Gly Glu Phe Ser Arg Ala Leu Ala Leu Glu
605 610 615

Val Gly Ser Ser Gln Phe Asn Asn Glu Ser Leu Leu Phe Phe Cys
620 625 630

Asp Val Asp Leu Val Phe Thr Thr Glu Phe Leu Gln Arg Cys Arg
635 640 645

Ala Asn Thr Val Leu Gly Gln Gln Ile Tyr Phe Pro Ile Ile Phe
650 655 660

Ser Gln Tyr Asp Pro Lys Ile Val Tyr Ser Gly Lys Val Pro Ser
665 670 675

Asp Asn His Phe Ala Phe Thr Gln Lys Thr Gly Phe Trp Arg Asn
680 685 690

Tyr Gly Phe Gly Ile Thr Cys Ile Tyr Lys Gly Asp Leu Val Arg
695 700 705

Val Gly Gly Phe Asp Val Ser Ile Gln Gly Trp Gly Leu Glu Asp
710 715 720

Val Asp Leu Phe Asn Lys Val Val Gln Ala Gly Leu Lys Thr Phe
725 730 735

Arg Ser Gln Glu Val Gly Val Val His Val His His Pro Val Phe
740 745 750

Cys Asp Pro Asn Leu Asp Pro Lys Gln Tyr Lys Met Cys Leu Gly
755 760 765

Ser Lys Ala Ser Thr Tyr Gly Ser Thr Gln Gln Leu Ala Glu Met

770 775 780

Trp Leu Glu Lys Asn Asp Pro Ser Tyr Ser Lys Ser Ser Asn Asn
785 790 795

Asn Gly Ser Val Arg Thr Ala
800

<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 261

gtgccactac ggggtgtgga cgac 24

<210> 262

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 262

tcccatttct tccgtggtgc ccag 24

<210> 263

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 263

ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264

<211> 1419

<212> DNA

<213> Homo sapiens

<400> 264

ggacaaccgt tgctgggtgt cccagggcct gaggcaggac ggtactccgc 50

tgacaccttc ccttcggcc ttgaggtcc cagcctggtg gccccaggac 100

gttcgggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150

tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200

agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250

agttttagag aacctagtac gaagtgtcc ctctggggag ccaggtcgtg 300

agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350

tcaaaattta aggagctagt tacacatgga gacgctcaa ctgagaatga 400

tgttttaacc aatcctatca gtgaagaaac tacaacttc cctacaggag 450

ggttcacacc ggaatagga aagaaaaaac acacggaaag taccccatc 500

tggtcgtatca aaccaaacaa tggttccatt gttttgcatg cagaggaacc 550

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ccatatgtta cctcatataa gtcacctgtc accactttag ataagagcac 700

tggcattgag atctctacag aatcagaaga tgttctcag ctctcaggtg 750

aaactgcat agaaaaacc gaagagtttg gaaagcacc agagagttgg 800

aataatgatg acattttgaa aaaaatttta gatattaatt cacaagtgc 850

acaggcactt cttagtaca ccagcaacc agcatataga gaagatattg 900

aagcctctaa agatcaccta aaacgaagcc ttgctctagc agcagcagca 950

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aacaagtaat aaaattgatg acatcgaaac tgttattaac atgctgtgta 1050

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attttggttc aggaaaaaa 1419

<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met Lys Pro Leu Val Leu Leu Val Ala Leu Leu Leu Trp Pro Ser

1 5 10 15

Ser Val Pro Ala Tyr Pro Ser Ile Thr Val Thr Pro Asp Glu Glu

20 25 30

Gln Asn Leu Asn His Tyr Ile Gln Val Leu Glu Asn Leu Val Arg

35 40 45

Ser Val Pro Ser Gly Glu Pro Gly Arg Glu Lys Lys Ser Asn Ser

50 55 60

Pro Lys His Val Tyr Ser Ile Ala Ser Lys Gly Ser Lys Phe Lys

65 70 75

Glu Leu Val Thr His Gly Asp Ala Ser Thr Glu Asn Asp Val Leu

80 85 90

Thr Asn Pro Ile Ser Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly

95	100	105
Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro		
110	115	120
Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala		
125	130	135
Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu		
140	145	150
Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val		
155	160	165
Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro		
170	175	180
Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu		
185	190	195
Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys		
200	205	210
Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp		
215	220	225
Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala		
230	235	240
Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu		
245	250	255
Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala		
260	265	270
Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro		
275	280	285
Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile		
290	295	300
Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp		
305	310	315

Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val
320 325 330

Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala
335 340 345

Leu Leu Lys Val Tyr
350

<210> 266

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 266

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ttcatagtgt gagatcaacc cacaggaata tccatggctt ttgtgctcat 150

tttggtctc agtttctacg agctgggtgc aggacagtgg caagtcactg 200

gaccgggcaa gttgtccag gccttgggtg gggaggacgc cgtgttctcc 250

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 gtaattcagc acattaataa agtaaaaaag aaaaccataa aaaaaaaaaa 2400
 aaa 2403

<210> 267
 <211> 466
 <212> PRT
 <213> Homo sapiens

<400> 267
 Met Ala Phe Val Leu Ile Leu Val Leu Ser Phe Tyr Glu Leu Val
 1 5 10 15
 Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala
 20 25 30
 Leu Val Gly Glu Asp Ala Val Phe Ser Cys Ser Leu Phe Pro Glu
 35 40 45
 Thr Ser Ala Glu Ala Met Glu Val Arg Phe Phe Arg Asn Gln Phe
 50 55 60

His Ala Val Val His Leu Tyr Arg Asp Gly Glu Asp Trp Glu Ser
65 70 75

Lys Gln Met Pro Gln Tyr Arg Gly Arg Thr Glu Phe Val Lys Asp
80 85 90

Ser Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr
95 100 105

Pro Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Gln Ile
110 115 120

Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly
125 130 135

Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile
140 145 150

Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Gln Pro Thr Ala
155 160 165

Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Ser Asp Ser Arg
170 175 180

Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile
185 190 195

Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu
200 205 210

Ala Glu Gln Ser His Glu Val Glu Ser Lys Val Leu Ile Gly Glu
215 220 225

Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu
230 235 240

Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile
245 250 255

Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp
260 265 270

Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys

275	280	285
His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys		
290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro		
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val		
320	325	330
Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val		
335	340	345
Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp		
350	355	360
Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn		
365	370	375
Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr		
380	385	390
Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr		
395	400	405
Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe		
410	415	420
Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys		
425	430	435
Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr		
440	445	450
Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp		
455	460	465

Gly

<210> 268

<211> 2103

<212> DNA

<213> Homo sapiens

<400> 268

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tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250
aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300
atttataaa tctccattaa gggaagaatt tgtcaagtct caggttatca 350
agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400
agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact 450
tgttttacat gaaaagctgc aagatgctgt aggaccccct aaagtagatc 500
ctcactcagt taaaattaaa aaaatcaaca agacagaaac agacagctat 550
ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600
caggatcgtt ggtgggacag aagtagaaga gggatgaatgg ccctggcagg 650
ctagcctgca gtgggatggg agtcacgctg gtggagcaac cttaattaat 700
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tatgtgctgg ctccctagaa ggaaaaacag atgcatgcca gggtgactct 1150
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cca 2103

<210> 269

<211> 423

<212> PRT

<213> Homo sapiens

<400> 269

Met Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys

1 5 10 15

Trp Glu Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile

20 25 30

Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr

35 40 45

Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr

50 55 60

Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn

65 70 75

Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala

80 85 90

Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val

95 100 105

Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu

110 115 120

Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp

125 130 135

Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val

140 145 150

Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile

155 160 165

Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr

170 175 180

Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
185 190 195

Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
200 205 210

Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
215 220 225

Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro
230 235 240

Ala Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys
245 250 255

Met Lys Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys
260 265 270

His Pro Ser His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser
275 280 285

Pro Val Pro Tyr Thr Asn Ala Val His Arg Val Cys Leu Pro Asp
290 295 300

Ala Ser Tyr Glu Phe Gln Pro Gly Asp Val Met Phe Val Thr Gly
305 310 315

Phe Gly Ala Leu Lys Asn Asp Gly Tyr Ser Gln Asn His Leu Arg
320 325 330

Gln Ala Gln Val Thr Leu Ile Asp Ala Thr Thr Cys Asn Glu Pro
335 340 345

Gln Ala Tyr Asn Asp Ala Ile Thr Pro Arg Met Leu Cys Ala Gly
350 355 360

Ser Leu Glu Gly Lys Thr Asp Ala Cys Gln Gly Asp Ser Gly Gly
365 370 375

Pro Leu Val Ser Ser Asp Ala Arg Asp Ile Trp Tyr Leu Ala Gly
380 385 390

Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro Asn Lys Pro Gly

395 400 405

Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile Thr Ser Lys

410 415 420

Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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cagacgtcag ctggtggatt cccgctgcat caaggcctac ccaactgtctc 150

catgctgggc tctccctgcc ttctgtggct cctggccgtg accttcttgg 200

ttcccagagc tcagcccttg gccctcaag actttgaaga agaggaggca 250

gatgagactg agacggcgtg gccgccttg ccggctgtcc cctgcgacta 300

cgaccactgc cgacacctgc aggtgccctg caaggagcta cagagggtcg 350

ggccggcggc ctgcctgtgc ccaggactct ccagccccgc ccagccgccc 400

gacccgccgc gcatgggaga agtgcgcatl gcggccgaag agggccgcgc 450

agtgtccac tgggtgtccc ctttctccc ggtcctccac tactggctgc 500

tgttttggga cggcagcgag gctgcgcaga aggggcccc gctgaacgct 550

acggtccgca gagccgaact gaaggggctg aagccagggg gcatttatgt 600

cgtttgcgta gtggccgcta acgaggccgg ggcaagccgc gtgccccagg 650

ctggaggaga gggcctcgag ggggcccaca tcctgcctt cgggccttgc 700

agccgccttg cgggtccgcc caacccccgc actctggtcc acgcggccgt 750

cggggtgggc acggccctgg ccctgctaag ctgtgccgcc ctggtgtggc 800
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 cccacactgg ggcgtcagc ctggcccccg ggaaagagga aaaccgctg 950
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 gccacggcgg agtcatggtt ctcaggactg agcgcttgtt taggtccggt 1050
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 cccaatttt ttttaagcg gccagataat aaataatga accttgcgg 1150
 ttaaaaaaaaa aaaaaaaaaa 1170

<210> 271

<211> 238

<212> PRT

<213> Homo sapiens

<400> 271

Met Leu Gly Ser Pro Cys Leu Leu Trp Leu Leu Ala Val Thr Phe

1 5 10 15

Leu Val Pro Arg Ala Gln Pro Leu Ala Pro Gln Asp Phe Glu Glu

20 25 30

Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala

35 40 45

Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys

50 55 60

Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly

65 70 75

Leu Ser Ser Pro Ala Gln Pro Pro Asp Pro Pro Arg Met Gly Glu

80 85 90

Val Arg Ile Ala Ala Glu Glu Gly Arg Ala Val Val His Trp Cys

95	100	105
Ala Pro Phe Ser Pro Val Leu His Tyr Trp Leu Leu Leu Trp Asp		
110	115	120
Gly Ser Glu Ala Ala Gln Lys Gly Pro Pro Leu Asn Ala Thr Val		
125	130	135
Arg Arg Ala Glu Leu Lys Gly Leu Lys Pro Gly Gly Ile Tyr Val		
140	145	150
Val Cys Val Val Ala Ala Asn Glu Ala Gly Ala Ser Arg Val Pro		
155	160	165
Gln Ala Gly Gly Glu Gly Leu Glu Gly Ala Asp Ile Pro Ala Phe		
170	175	180
Gly Pro Cys Ser Arg Leu Ala Val Pro Pro Asn Pro Arg Thr Leu		
185	190	195
Val His Ala Ala Val Gly Val Gly Thr Ala Leu Ala Leu Leu Ser		
200	205	210
Cys Ala Ala Leu Val Trp His Phe Cys Leu Arg Asp Arg Trp Gly		
215	220	225
Cys Pro Arg Arg Ala Ala Ala Arg Ala Ala Gly Ala Leu		
230	235	

<210> 272

<211> 2397

<212> DNA

<213> Homo sapiens

<400> 272

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cccaggcggg cgtggggcac cgggccagc gccgacgac gctgccgttt 150

tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200

gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgcctgctct 250
acgccctcaa tctgtctttt tggtaatgt ccatcagtgt gttggcagtt 300
tctgcttgga tgagggacta cctaaataat gttctcactt taactgcaga 350
aacgagggta gaggaagcag tcattttgac ttactttcct gtggttcatt 400
cggtcattgat tgctgtttgc tgtttcctta tcattgtggg gatgttagga 450
tattgtggaa cggtgaaaag aaatctgttg cttcttgcatt ggtactttgg 500
aagtttgctt gtcattttct gtgtagaact ggcttggtgc gtttgacat 550
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tactgactg gttggaaatg acagagatgg actggcccc agattcctgc 750
tgtgttagag aattcccagg atgttccaaa caggcccacc aggaagatct 800
cagtgcattt tatcaagagg gttgtgggaa gaaaatgat tcctttttga 850
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cagaaatatg tagaaataaa aatgttgcca taaaataaca cctaagcata 1250
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ctcttttga cactaaacac ttttaaaaa gcttatctt gccttctcca 2100

aacaagaagc aatagtctcc aagtcaatat aaattctaca gaaaatagt 2150

ttcttttct ccagaaaaat gcttgagaga atcattaaaa catgtgacaa 2200

tttagagatt cttgtttta tticactgat taatatactg tggcaaatta 2250

cacagattat taaattttt tacaagagta tagtatattt atttgaaatg 2300

ggaaaagtgc atttactgt attttgtga tttgtttat ttctcagaat 2350

atggaaagaa aattaaaatg tgtcaataaa tattttctag agagtaa 2397

<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

Met Ala Arg Glu Asp Ser Val Lys Cys Leu Arg Cys Leu Leu Tyr
1 5 10 15

Ala Leu Asn Leu Leu Phe Trp Leu Met Ser Ile Ser Val Leu Ala
20 25 30

Val Ser Ala Trp Met Arg Asp Tyr Leu Asn Asn Val Leu Thr Leu
35 40 45

Thr Ala Glu Thr Arg Val Glu Glu Ala Val Ile Leu Thr Tyr Phe
50 55 60

Pro Val Val His Pro Val Met Ile Ala Val Cys Cys Phe Leu Ile
65 70 75

Ile Val Gly Met Leu Gly Tyr Cys Gly Thr Val Lys Arg Asn Leu
80 85 90

Leu Leu Leu Ala Trp Tyr Phe Gly Ser Leu Leu Val Ile Phe Cys
95 100 105

Val Glu Leu Ala Cys Gly Val Trp Thr Tyr Glu Gln Glu Leu Met
110 115 120

Val Pro Val Gln Trp Ser Asp Met Val Thr Leu Lys Ala Arg Met
125 130 135

Thr Asn Tyr Gly Leu Pro Arg Tyr Arg Trp Leu Thr His Ala Trp
140 145 150

Asn Phe Phe Gln Arg Glu Phe Lys Cys Cys Gly Val Val Tyr Phe
155 160 165

Thr Asp Trp Leu Glu Met Thr Glu Met Asp Trp Pro Pro Asp Ser
170 175 180

Cys Cys Val Arg Glu Phe Pro Gly Cys Ser Lys Gln Ala His Gln

185	190	195
Glu Asp Leu Ser Asp Leu Tyr Gln Glu Gly Cys Gly Lys Lys Met		
200	205	210
Tyr Ser Phe Leu Arg Gly Thr Lys Gln Leu Gln Val Leu Arg Phe		
215	220	225
Leu Gly Ile Ser Ile Gly Val Thr Gln Ile Leu Ala Met Ile Leu		
230	235	240
Thr Ile Thr Leu Leu Trp Ala Leu Tyr Tyr Asp Arg Arg Glu Pro		
245	250	255
Gly Thr Asp Gln Met Met Ser Leu Lys Asn Asp Asn Ser Gln His		
260	265	270
Leu Ser Cys Pro Ser Val Glu Leu Leu Lys Pro Ser Leu Ser Arg		
275	280	285
Ile Phe Glu His Thr Ser Met Ala Asn Ser Phe Asn Thr His Phe		
290	295	300
Glu Met Glu Glu Leu		
305		

<210> 274

<211> 2063

<212> DNA

<213> Homo sapiens

<400> 274

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ttctgacctg ctggccagcc aggacctgtg tggggaggcc ctctgctgc 150

cttgggtga caatctcage tccaggctac agggagaccg ggaggatcac 200

agagccagca tgttacagga tcctgacagt gatcaacctc tgaacagcct 250

cgatgtcaaa cccctgcgca aaccccgat ccccatggag accttcagaa 300

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<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp

1 5 10 15

Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg

20 25 30

Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser

35 40 45

Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr
50 55 60

Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
65 70 75

Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu
80 85 90

His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg
95 100 105

Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr
110 115 120

Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu
125 130 135

Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu
140 145 150

Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn
155 160 165

Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser
170 175 180

Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu
185 190 195

Lys Thr Pro Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser
200 205 210

Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys
215 220 225

Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His
230 235 240

Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala
245 250 255

Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala Val Ala Lys

260	265	270
Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp Asn Asp		
275	280	285
Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly Thr		
290	295	300
Val Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro		
305	310	315
Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn		
320	325	330
Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val		
335	340	345
Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu		
350	355	360
Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val		
365	370	375
Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser		
380	385	390
Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys		
395	400	405
Gly Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr		
410	415	420
Leu Asn Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu		
425	430	

<210> 276

<211> 3143

<212> DNA

<213> Homo sapiens

<400> 276

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gagcatggcc ctcccagccc tgggcctgga cccctggagc ctctggggcc 150
ttttctctt ccaactgctt cagctgctgc tgccgacgac gaccgcgggg 200
ggaggcgggc aggggccc at gccagggc agatactatg caggggatga 250
acgtagggca cttagcttct tccaccagaa gggcctccag gattttgaca 300
ctctgctct gagtggatg ggaaatactc tctacgtggg ggctcgagaa 350
gccattctgg ccttgatat ccaggatcca ggggtcccca ggctaaagaa 400
catgataccg tggccagcca gtgacagaaa aaagagtga tgtgcctta 450
agaagaagag caatgagaca cagtgttca acttcatccg tgtctggtt 500
tcttacaatg tcacccatct ctacacctgc ggcacctcg ccttcagccc 550
tgcttgacc ttcatgaac ttcaagattc ctacctgtg cccatctcg 600
aggacaaggt catggaggga aaaggccaaa gccccttga ccccgctcac 650
aagcatacgg ctgtcttggg gatgggatg ctctattctg gtactatga 700
caacttctg ggcagtgagc ccatctgat gcgcacactg ggatcccagc 750
ctgtctcaa gaccgacaac ttctccgct ggctgcatca tgacgcctcc 800
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<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

Met Ala Leu Pro Ala Leu Gly Leu Asp Pro Trp Ser Leu Leu Gly

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20	25	30	
Ala Gly Gly Gly Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Tyr			
35	40	45	
Ala Gly Asp Glu Arg Arg Ala Leu Ser Phe Phe His Gln Lys Gly			
50	55	60	
Leu Gln Asp Phe Asp Thr Leu Leu Leu Ser Gly Asp Gly Asn Thr			
65	70	75	
Leu Tyr Val Gly Ala Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln			
80	85	90	
Asp Pro Gly Val Pro Arg Leu Lys Asn Met Ile Pro Trp Pro Ala			
95	100	105	
Ser Asp Arg Lys Lys Ser Glu Cys Ala Phe Lys Lys Lys Ser Asn			
110	115	120	
Glu Thr Gln Cys Phe Asn Phe Ile Arg Val Leu Val Ser Tyr Asn			
125	130	135	
Val Thr His Leu Tyr Thr Cys Gly Thr Phe Ala Phe Ser Pro Ala			
140	145	150	
Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr Leu Leu Pro Ile Ser			
155	160	165	
Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser Pro Phe Asp Pro			
170	175	180	
Ala His Lys His Thr Ala Val Leu Val Asp Gly Met Leu Tyr Ser			
185	190	195	
Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu Met Arg			
200	205	210	
Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu Arg			
215	220	225	

Trp Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr
230 235 240

Gln Val Val Tyr Phe Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp
245 250 255

Phe Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys
260 265 270

Asn Asp Val Gly Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Thr
275 280 285

Phe Leu Lys Ala Gln Leu Leu Cys Thr Gln Pro Gly Gln Leu Pro
290 295 300

Phe Asn Val Ile Arg His Ala Val Leu Leu Pro Ala Asp Ser Pro
305 310 315

Thr Ala Pro His Ile Tyr Ala Val Phe Thr Ser Gln Trp Gln Val
320 325 330

Gly Gly Thr Arg Ser Ser Ala Val Cys Ala Phe Ser Leu Leu Asp
335 340 345

Ile Glu Arg Val Phe Lys Gly Lys Tyr Lys Glu Leu Asn Lys Glu
350 355 360

Thr Ser Arg Trp Thr Thr Tyr Arg Gly Pro Glu Thr Asn Pro Arg
365 370 375

Pro Gly Ser Cys Ser Val Gly Pro Ser Ser Asp Lys Ala Leu Thr
380 385 390

Phe Met Lys Asp His Phe Leu Met Asp Glu Gln Val Val Gly Thr
395 400 405

Pro Leu Leu Val Lys Ser Gly Val Glu Tyr Thr Arg Leu Ala Val
410 415 420

Glu Thr Ala Gln Gly Leu Asp Gly His Ser His Leu Val Met Tyr
425 430 435

Leu Gly Thr Thr Thr Gly Ser Leu His Lys Ala Val Val Ser Gly

440	445	450
Asp Ser Ser Ala His Leu Val Glu Glu Ile Gln Leu Phe Pro Asp		
455	460	465
Pro Glu Pro Val Arg Asn Leu Gln Leu Ala Pro Thr Gln Gly Ala		
470	475	480
Val Phe Val Gly Phe Ser Gly Gly Val Trp Arg Val Pro Arg Ala		
485	490	495
Asn Cys Ser Val Tyr Glu Ser Cys Val Asp Cys Val Leu Ala Arg		
500	505	510
Asp Pro His Cys Ala Trp Asp Pro Glu Ser Arg Thr Cys Cys Leu		
515	520	525
Leu Ser Ala Pro Asn Leu Asn Ser Trp Lys Gln Asp Met Glu Arg		
530	535	540
Gly Asn Pro Glu Trp Ala Cys Ala Ser Gly Pro Met Ser Arg Ser		
545	550	555
Leu Arg Pro Gln Ser Arg Pro Gln Ile Ile Lys Glu Val Leu Ala		
560	565	570
Val Pro Asn Ser Ile Leu Glu Leu Pro Cys Pro His Leu Ser Ala		
575	580	585
Leu Ala Ser Tyr Tyr Trp Ser His Gly Pro Ala Ala Val Pro Glu		
590	595	600
Ala Ser Ser Thr Val Tyr Asn Gly Ser Leu Leu Leu Ile Val Gln		
605	610	615
Asp Gly Val Gly Gly Leu Tyr Gln Cys Trp Ala Thr Glu Asn Gly		
620	625	630
Phe Ser Tyr Pro Val Ile Ser Tyr Trp Val Asp Ser Gln Asp Gln		
635	640	645
Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly Ile Pro Arg Glu His		
650	655	660

Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly Ala Ala Leu Ala
665 670 675

Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val Thr Val Leu
680 685 690

Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val Ala Ser
695 700 705

Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys Glu
710 715 720

Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His
725 730 735

Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp
740 745 750

Ala Asp Asn Asn Cys Leu Gly Thr Glu Val Ala
755 760

<210> 278

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 278

ctgctggtga aatctggcgt ggag 24

<210> 279

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 279

gtctggtcct ggctgtccac ccag 24

<210> 280

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 280

catcttgta tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281

<211> 2320

<212> DNA

<213> Homo sapiens

<400> 281

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cttccgtaga agtgagcatg gctgggcagc gaggcttct tctagtgggc 100

ttcttctcc ctggggctct gctctcagag gctgcaaaa tctgacaat 150

atctacagta ggtggaagcc attatctact gatggaccgg gtttctaga 200

ttctcaaga tcacggcat aatgtacca tgcttaacca caaaagagg 250

ccttttatgc cagatttta aaaggaagaa aaatcatatc aagttatcag 300

ttggcttgca cctgaagatc atcaaagaga atttaaaaag agtttgatt 350

tcttctgga agaaacttta ggtggcagag gaaaattga aaactatta 400

aatgttctag aatacttggc gttgcagtgc agtcatttt taaatagaaa 450

ggatatcatg gattccttaa agaagagaa ctgcacatg gtgatagttg 500

aaactttga ctactgtct ttcctgattg ctgagaagct tggaagcca 550

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 tctctccca acctactaa 2320

<210> 282

<211> 523

<212> PRT

<213> Homo sapiens

<400> 282

Met Ala Gly Gln Arg Val Leu Leu Leu Val Gly Phe Leu Leu Pro

1 5 10 15

Gly Val Leu Leu Ser Glu Ala Ala Lys Ile Leu Thr Ile Ser Thr

20 25 30

Val Gly Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile

35 40 45

Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg

50 55 60

Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln

65	70	75
Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys		
80	85	90
Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly		
95	100	105
Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln		
110	115	120
Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys		
125	130	135
Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys		
140	145	150
Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile		
155	160	165
Leu Ser Thr Ser Phe Gly Ser Leu Glu Phe Gly Leu Pro Ile Pro		
170	175	180
Leu Ser Tyr Val Pro Val Phe Arg Ser Leu Leu Thr Asp His Met		
185	190	195
Asp Phe Trp Gly Arg Val Lys Asn Phe Leu Met Phe Phe Ser Phe		
200	205	210
Cys Arg Arg Gln Gln His Met Gln Ser Thr Phe Asp Asn Thr Ile		
215	220	225
Lys Glu His Phe Thr Glu Gly Ser Arg Pro Val Leu Ser His Leu		
230	235	240
Leu Leu Lys Ala Glu Leu Trp Phe Ile Asn Ser Asp Phe Ala Phe		
245	250	255
Asp Phe Ala Arg Pro Leu Leu Pro Asn Thr Val Tyr Val Gly Gly		
260	265	270
Leu Met Glu Lys Pro Ile Lys Pro Val Pro Gln Asp Leu Glu Asn		
275	280	285

Phe Ile Ala Lys Phe Gly Asp Ser Gly Phe Val Leu Val Thr Leu
290 295 300

Gly Ser Met Val Asn Thr Cys Gln Asn Pro Glu Ile Phe Lys Glu
305 310 315

Met Asn Asn Ala Phe Ala His Leu Pro Gln Gly Val Ile Trp Lys
320 325 330

Cys Gln Cys Ser His Trp Pro Lys Asp Val His Leu Ala Ala Asn
335 340 345

Val Lys Ile Val Asp Trp Leu Pro Gln Ser Asp Leu Leu Ala His
350 355 360

Pro Ser Ile Arg Leu Phe Val Thr His Gly Gly Gln Asn Ser Ile
365 370 375

Met Glu Ala Ile Gln His Gly Val Pro Met Val Gly Ile Pro Leu
380 385 390

Phe Gly Asp Gln Pro Glu Asn Met Val Arg Val Glu Ala Lys Lys
395 400 405

Phe Gly Val Ser Ile Gln Leu Lys Lys Leu Lys Ala Glu Thr Leu
410 415 420

Ala Leu Lys Met Lys Gln Ile Met Glu Asp Lys Arg Tyr Lys Ser
425 430 435

Ala Ala Val Ala Ala Ser Val Ile Leu Arg Ser His Pro Leu Ser
440 445 450

Pro Thr Gln Arg Leu Val Gly Trp Ile Asp His Val Leu Gln Thr
455 460 465

Gly Gly Ala Thr His Leu Lys Pro Tyr Val Phe Gln Gln Pro Trp
470 475 480

His Glu Gln Tyr Leu Phe Asp Val Phe Val Phe Leu Leu Gly Leu
485 490 495

Thr Leu Gly Thr Leu Trp Leu Cys Gly Lys Leu Leu Gly Met Ala

500

505

510

Val Trp Trp Leu Arg Gly Ala Arg Lys Val Lys Glu Thr
515 520

<210> 283

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 283

tgcccttgct cacctacccc aagg 24

<210> 284

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 284

tcaggctggt ctccaaagag aggg 24

<210> 285

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 285

cccaaagatg tccacctggc tgcaaatgtg aaaattgtgg actgg 45

<210> 286

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 286

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caactagaga atggtgtgtca gtgagacact atagaattac taaggagaag 2250

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agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met Leu Gly Ala Lys Pro His Trp Leu Pro Gly Pro Leu His Ser

1 5 10 15

Pro Gly Leu Pro Leu Val Leu Val Leu Leu Ala Leu Gly Ala Gly

20 25 30

Trp Ala Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys

35 40 45

Leu Val Val Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly

50 55 60

Gly Ala Ala Leu Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Ala

65 70 75

Ala Val Arg Ser His His His Glu Pro Ala Gly Glu Thr Gly Asn

80 85 90

Gly Thr Ser Gly Ala Ile Tyr Phe Asp Gln Val Leu Val Asn Glu

95 100 105

Gly Gly Gly Phe Asp Arg Ala Ser Gly Ser Phe Val Ala Pro Val

110 115 120

Arg Gly Val Tyr Ser Phe Arg Phe His Val Val Lys Val Tyr Asn

125 130 135

Arg Gln Thr Val Gln Val Ser Leu Met Leu Asn Thr Trp Pro Val

140 145 150

Ile Ser Ala Phe Ala Asn Asp Pro Asp Val Thr Arg Glu Ala Ala
155 160 165

Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly Asp Arg Val Ser
170 175 180

Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser
185 190 195

Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu
200 205

<210> 288

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 288

aggcagccac cagctctgtg ctac 24

<210> 289

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 289

cagagagggga agatgaggaa gccagag 27

<210> 290

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 290

ctgtgtact gcccttgac cctggggacc gagggtct gc 42

<210> 291

<211> 1570

<212> DNA

<213> Homo sapiens

<400> 291

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ttcccgccc gccgtgactg ggcgggcttc agccatgaag accctcatag 200

ccgcctactc cggggctctg cgcggcgagc gtcaggccga ggctgaccgg 250

agccagcgt ctcacggagg acctgcgctg tcgcgcgagg ggtctgggag 300

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tcacctggct caataggtcc aagggtgaaa agcagctaca ggtcatctca 400

gtgtccagt gggctctgtc ctctctgta ctgggagtgg cctgcagtgc 450

catcctcatg tacatattct gactgattg ctggctcatc gctgtgtct 500

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atatcttgg ataccacccc catggtatca tgggcctggg tgcttctgc 700

aacttcagca cagaggccac agaagtgagc aagaagtcc caggcatacg 750

gccttacctg gctacactgg caggcaactt ccgaatgcct gtgttgaggg 800

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tatttgctt caaagaatgg gagggtgcaat gctatcatca tcgtggtcgg 900

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<210> 292

<211> 388

<212> PRT

<213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu
1		5			10				15					

Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro
	20			25				30						

Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser
	35				40				45					

Ile Leu Ser Ala Leu Gln Asp Leu Phe Ser Val Thr Trp Leu Asn
50 55 60

Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln
65 70 75

Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Ala Ile
80 85 90

Leu Met Tyr Ile Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu
95 100 105

Tyr Phe Thr Trp Leu Val Phe Asp Trp Asn Thr Pro Lys Lys Gly
110 115 120

Gly Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr
125 130 135

Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu
140 145 150

Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile
155 160 165

Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu
170 175 180

Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu
185 190 195

Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser
200 205 210

Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu
215 220 225

Ser Lys Asn Gly Ser Gly Asn Ala Ile Ile Ile Val Val Gly Gly
230 235 240

Ala Ala Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr
245 250 255

Leu Arg Asn Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly

260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr		
275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln		
290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His		
305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr		
320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro		
335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr		
350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr		
365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn		
380	385	

<210> 293

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

gctgacctgg ttccatcta ctcc 24

<210> 294

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cccacagaca cccatgacac ttcc 24

<210> 295

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 295

aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296

<211> 3060

<212> DNA

<213> Homo sapiens

<400> 296

gggcggcggg atggggggcgg ggggcggcgg gcgccgcact cgctgaggcc 50

ccgacgcagg gccggggcgg gccagggcc gaggagcgcg gcggccagag 100

cgggggccgc gaggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150

gcggctgcag gcttgccag ccggaagccc tgagggcagc tgtcccact 200

ggctctgctg accttgctcc ttggacggct gtcctcagcg aggggccgtg 250

caccgcctcc tgagcagcgc catgggcctg ctggccttc tgaagacca 300

gttcgtgctg cacctgctgg tcggctttgt ctctgtgtg agtggctg 350

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aaccttcaac tgaattatt ggacttttga gtcttagatg gtcctgacct 2000
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<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu

1 5 10 15

Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe

20 25 30

Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu

35 40 45

Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln

50 55 60

Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu

65 70 75

Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala

80 85 90

Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly

95 100 105

Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val

110 115 120

Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr
125 130 135

Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu
140 145 150

Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr
155 160 165

Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe
170 175 180

Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala Lys
185 190 195

Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly
200 205 210

Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val
215 220 225

Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu
230 235 240

Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val
245 250 255

Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala
260 265 270

Ala Gln Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln
275 280 285

Glu Ile Tyr Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys
290 295 300

Pro Ala Arg Arg Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala
305 310 315

Thr Ile Leu Leu Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe
320 325 330

Ala Ser Gly Ser Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val

335 340 345

Gly Ala Ala Ser Phe Gly Val Arg Arg Leu Ile Gly Glu Ser Leu

350 355 360

Glu Pro Gly Arg Trp Arg Leu Gln

365

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 298

cttctctctgt ggggtggacca tgtg 24

<210> 299

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 299

gccacctcca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 300

ccaaggtcct cgctaagaag gagctgctct acgtgccct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

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tgtcttgggg cagccaccag gcatattcat ctttgtgtgt gttttcttt 100
tgcttttagca ctggggcact tcttgcttat ttctttgga ggaaaggggc 150
tcagtttgc ttgtgggggt ggtggcaggc aggccggctt acgcctgata 200
cggccctggg ttagaaggga agggaagata aactttata caaatgggga 250
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 gtcccagcta cttgggaggc tgaagcaaga gaatcgcttg aacctgggag 1250
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 acagagtgag actctatgtc caaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met His His Ser Leu Gln Cys Pro Gly Ala Ala Thr Arg His Ile

1 5 10 15

His Leu Cys Val Cys Phe Ser Phe Ala Leu Ala Leu Gly His Phe

20 25 30

Leu Leu Ile Ser Leu Val Gly Lys Gly Leu Ser Leu Ser Cys Gly

35 40 45

Val Gly Gly Arg Gln Ala Gly Leu Arg Leu Ile Arg Pro Trp Val

50 55 60

Arg Arg Glu Gly Lys Ile Asn Phe Tyr Thr Asn Gly Asp Ser Trp

65 70 75

Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr

80 85 90

Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln

95 100 105

Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu

110 115 120

Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr
125 130 135

Cys Gly Val Leu Leu Ser Phe Leu
140

<210> 303

<211> 1768

<212> DNA

<213> Homo sapiens

<400> 303

ggctggactg gaactcctgg tcccaagtga tccaccgcc tcagctccc 50

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ttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150

tatgctgtgg tggctagtgc tcctactcct acctacatta aaatctgtt 200

ttgttctct tgtaactagc cttfaccttc ctaacacaga ggatctgtca 250

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tttaccac accgtccct cgaagccggg gacagctca cttgctggc 350

ctctcgtgg agcagtgcct tcaccaactg tctcacgtct ggaggcactg 400

actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg 450

tgggcctgc cctggccgta gaagggattg acaagcccga agatttcata 500

ggcgtggct cccactgccc aggcacgacg cttgctgtag tcaatcactg 550

ccctggggcc aggacgggcc gtggacacct gctcagaagc agtgggtgag 600

acatcacgt gcccgcccat ctaaccttt catgtctgc acatcacctg 650

atccatgggc taatctgaac tctgtccaa ggaaccaga gcttgagtga 700

gctgtggctc agaccagaa ggggtctgct tagaccacct ggtttatgtg 750

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gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700
ttcagcctga gcaacacagc gagactctgt ctcagaaaaa ataaaaaag 1750
aattatggtt atttgtaa 1768

<210> 304

<211> 109

<212> PRT

<213> Homo sapiens

<400> 304

Met Leu Trp Trp Leu Val Leu Leu Leu Pro Thr Leu Lys Ser

1 5 10 15

Val Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu

20 25 30

Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly

35 40 45

Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly

50 55 60

Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro

65 70 75

Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala

80 85 90

Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly

95 100 105

Arg Arg Arg Asp

<210> 305

<211> 989

<212> DNA

<213> Homo sapiens

<400> 305

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tgtcactgcc tcccgcgcgc tctgtcccgc gccatgaccc agccggtgcc 100

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ccgccttcgc cactggcctc ttctgggga ggcggtgccc cccatggcga 200

ggccggcgag agcagtgcct gcttcccccc gaggacagcc gcctgtggca 250

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 gagggttgcc tgggaacccc aggaattgac cctgagtttt aaattcgaaa 950
 ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

Met Thr Gln Pro Val Pro Arg Leu Ser Val Pro Ala Ala Leu Ala

1 5 10 15

Leu Gly Ser Ala Ala Leu Gly Ala Ala Phe Ala Thr Gly Leu Phe

20 25 30

Leu Gly Arg Arg Cys Pro Pro Trp Arg Gly Arg Arg Glu Gln Cys

35	40	45
Leu Leu Pro Pro Glu Asp Ser Arg Leu Trp Gln Tyr Leu Leu Ser		
50	55	60
Arg Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu		
65	70	75
Thr Leu Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln		
80	85	90
Ala Gln Leu Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys		
95	100	105
Ala Leu Asp Leu Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu		
110	115	120
Ala Leu Ala Leu Pro Ala Asp Gly Arg Val Val Thr Cys Glu Val		
125	130	135
Asp Ala Gln Pro Pro Glu Leu Gly Arg Pro Leu Trp Arg Gln Ala		
140	145	150
Glu Ala Glu His Lys Ile Asp Leu Arg Leu Lys Pro Ala Leu Glu		
155	160	165
Thr Leu Asp Glu Leu Leu Ala Ala Gly Glu Ala Gly Thr Phe Asp		
170	175	180
Val Ala Val Val Asp Ala Asp Lys Glu Asn Cys Ser Ala Tyr Tyr		
185	190	195
Glu Arg Cys Leu Gln Leu Leu Arg Pro Gly Gly Ile Leu Ala Val		
200	205	210
Leu Arg Val Leu Trp Arg Gly Lys Val Leu Gln Pro Pro Lys Gly		
215	220	225
Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu Arg Ile Arg		
230	235	240
Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly Asp Gly		
245	250	255

Leu Thr Leu Ala Phe Lys Ile
260

<210> 307

<211> 2272

<212> DNA

<213> Homo sapiens

<400> 307

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ggatggcgcc gtgaagcccc cacccaacaa gtaccccatc ttttttttg 200
gcacacaga aacagccttc ctgggaccca aggacctgtt ccctacgac 250
aaatgtaaag acaagtacgg gaagcccaac aagaggaaag gttcaatga 300
agggctgtgg gagatccaga acaaccccca cgccagctac agcgccctc 350
cgccagttag ctctccgac agcgaggccc ccgaggccaa ccccgccgac 400
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<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

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Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe

35 40 45

Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro

50 55 60

Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys

65 70 75

Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala

80 85 90

Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala

95 100 105

Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp

110 115 120

Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala	125	130	135
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Asp Asn Ser Gly Leu Lys Arg Lys Thr Pro Ala Leu Lys Met Ser	155	160	165
Val Ser Lys Arg Ala Arg Lys Ala Ser Ser Asp Leu Asp Gln Ala	170	175	180
Ser Val Ser Pro Ser Glu Glu Glu Asn Ser Glu Ser Ser Ser Glu	185	190	195
Ser Glu Lys Thr Ser Asp Gln Asp Phe Thr Pro Glu Lys Lys Ala	200	205	210
Ala Val Arg Ala Pro Arg Arg Gly Pro Leu Gly Gly Arg Lys Lys	215	220	225
Lys Lys Ala Pro Ser Ala Ser Asp Ser Asp Ser Lys Ala Asp Ser	230	235	240
Asp Gly Ala Lys Pro Glu Pro Val Ala Met Ala Arg Ser Ala Ser	245	250	255
Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Asp Val Ser Val	260	265	270
Lys Lys Pro Pro Arg Gly Arg Lys Pro Ala Glu Lys Pro Leu Pro	275	280	285
Lys Pro Arg Gly Arg Lys Pro Lys Pro Glu Arg Pro Pro Ser Ser	290	295	300
Ser Ser Ser Asp Ser Asp Ser Asp Glu Val Asp Arg Ile Ser Glu	305	310	315
Trp Lys Arg Arg Asp Glu Ala Arg Arg Arg Glu Leu Glu Ala Arg	320	325	330
Arg Arg Arg Glu Gln Glu Glu Glu Leu Arg Arg Leu Arg Glu Gln			

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Arg Gly Pro Pro Ser Ser Ser Asp Ser Glu Pro Glu Ala Glu Leu		
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Glu Arg Glu Ala Lys Lys Ser Ala Lys Lys Pro Gln Ser Ser Ser		
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Thr Glu Pro Ala Arg Lys Pro Gly Gln Lys Glu Lys Arg Val Arg		
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Cys Leu Asn Ala Leu Glu Glu Leu Gly Thr Leu Gln Val Thr Ser		
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Glu Val Tyr Thr Arg Leu Lys Ser Arg Val Leu Gly Pro Lys Ile		
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575 580 585

Pro Gln Glu Lys Ala Glu Asp Lys Pro Ser Thr Asp Leu Ser Ala
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Pro Val Asn Gly Glu Ala Thr Ser Gln Lys Gly Glu Ser Ala Glu
605 610 615

Asp Lys Glu His Glu Glu Gly Arg Asp Ser Glu Glu Gly Pro Arg
620 625 630

Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu Gly Pro
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<211> 3871

<212> DNA

<213> Homo sapiens

<400> 309

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<212> PRT

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<400> 310

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35 40 45

Lys Leu Thr Tyr Lys Asp Leu Leu Leu Ser Asn Ser Cys Ile Pro

50 55 60

Phe Leu Gly Ser Ser Glu Gly Leu Asp Phe Gln Thr Leu Leu Leu

65 70 75

Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

80 85 90

Phe Leu Leu Ser Leu Val Asp Leu Asn Lys Asn Phe Lys Lys Ile

95 100 105

Tyr Trp Pro Ala Ala Lys Glu Arg Val Glu Leu Cys Lys Leu Ala

110 115 120

Gly Lys Asp Ala Asn Thr Glu Cys Ala Asn Phe Ile Arg Val Leu

125 130 135

Gln Pro Tyr Asn Lys Thr His Ile Tyr Val Cys Gly Thr Gly Ala
140 145 150

Phe His Pro Ile Cys Gly Tyr Ile Asp Leu Gly Val Tyr Lys Glu
155 160 165

Asp Ile Ile Phe Lys Leu Asp Thr His Asn Leu Glu Ser Gly Arg
170 175 180

Leu Lys Cys Pro Phe Asp Pro Gln Gln Pro Phe Ala Ser Val Met
185 190 195

Thr Asp Glu Tyr Leu Tyr Ser Gly Thr Ala Ser Asp Phe Leu Gly
200 205 210

Lys Asp Thr Ala Phe Thr Arg Ser Leu Gly Pro Thr His Asp His
215 220 225

His Tyr Ile Arg Thr Asp Ile Ser Glu His Tyr Trp Leu Asn Gly
230 235 240

Ala Lys Phe Ile Gly Thr Phe Phe Ile Pro Asp Thr Tyr Asn Pro
245 250 255

Asp Asp Asp Lys Ile Tyr Phe Phe Phe Arg Glu Ser Ser Gln Glu
260 265 270

Gly Ser Thr Ser Asp Lys Thr Ile Leu Ser Arg Val Gly Arg Val
275 280 285

Cys Lys Asn Asp Val Gly Gly Gln Arg Ser Leu Ile Asn Lys Trp
290 295 300

Thr Thr Phe Leu Lys Ala Arg Leu Ile Cys Ser Ile Pro Gly Ser
305 310 315

Asp Gly Ala Asp Thr Tyr Phe Asp Glu Leu Gln Asp Ile Tyr Leu
320 325 330

Leu Pro Thr Arg Asp Glu Arg Asn Pro Val Val Tyr Gly Val Phe
335 340 345

Thr Thr Thr Ser Ser Ile Phe Lys Gly Ser Ala Val Cys Val Tyr

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Lys Glu Ser Ala Asp His Arg Trp Val Gln Tyr Asp Gly Arg Ile		
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Pro Tyr Pro Arg Pro Gly Thr Cys Pro Ser Lys Thr Tyr Asp Pro		
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Leu Ser Leu Lys Gln Gln Gln Leu Tyr Ile Gly Ser Arg Asp Gly		
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Leu Val Gln Leu Ser Leu His Arg Cys Asp Thr Tyr Gly Lys Ala		
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Gly Asn Ala Cys Ser Arg Tyr Ala Pro Thr Ser Lys Arg Arg Ala		
560	565	570

Arg Arg Gln Asp Val Lys Tyr Gly Asp Pro Ile Thr Gln Cys Trp
575 580 585

Asp Ile Glu Asp Ser Ile Ser His Glu Thr Ala Asp Glu Lys Val
590 595 600

Ile Phe Gly Ile Glu Phe Asn Ser Thr Phe Leu Glu Cys Ile Pro
605 610 615

Lys Ser Gln Gln Ala Thr Ile Lys Trp Tyr Ile Gln Arg Ser Gly
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Asp Glu His Arg Glu Glu Leu Lys Pro Asp Glu Arg Ile Ile Lys
635 640 645

Thr Glu Tyr Gly Leu Leu Ile Arg Ser Leu Gln Lys Lys Asp Ser
650 655 660

Gly Met Tyr Tyr Cys Lys Ala Gln Glu His Thr Phe Ile His Thr
665 670 675

Ile Val Lys Leu Thr Leu Asn Val Ile Glu Asn Glu Gln Met Glu
680 685 690

Asn Thr Gln Arg Ala Glu His Glu Glu Gly Gln Val Lys Asp Leu
695 700 705

Leu Ala Glu Ser Arg Leu Arg Tyr Lys Asp Tyr Ile Gln Ile Leu
710 715 720

Ser Ser Pro Asn Phe Ser Leu Asp Gln Tyr Cys Glu Gln Met Trp
725 730 735

His Arg Glu Lys Arg Arg Gln Arg Asn Lys Gly Gly Pro Lys Trp
740 745 750

Lys His Met Gln Glu Met Lys Lys Lys Arg Asn Arg Arg His His
755 760 765

Arg Asp Leu Asp Glu Leu Pro Arg Ala Val Ala Thr
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<210> 312
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Met Thr Gln Ala Gln Asp Glu Val Glu Gln Glu Arg Arg Leu Ser
95 100 105

Glu Ala Arg Leu Ser Gln Arg Asp Leu Ser Pro Thr Ala Glu Asp
110 115 120

Ala Glu Leu Ser Asp Phe Glu Glu Cys Glu Glu Thr Gly Glu Leu
125 130 135

Phe Glu Glu Pro Ala Pro Gln Ala Leu Ala Thr Arg Ala Leu Pro
140 145 150

Cys Pro Ala His Val Val Phe Arg Tyr Gln Ala Gly Arg Glu Asp
155 160 165

Glu Leu Thr Ile Thr Glu Gly Glu Trp Leu Glu Val Ile Glu Glu
170 175 180

Gly Asp Ala Asp Glu Trp Val Lys Ala Arg Asn Gln His Gly Glu
185 190 195

Val Gly Phe Val Pro Glu Arg Tyr Leu Asn Phe Pro Asp Leu Ser
200 205 210

Leu Pro Glu Ser Ser Gln Asp Ser Asp Asn Pro Cys Gly Ala Glu
215 220 225

Pro Thr Ala Phe Leu Ala Gln Ala Leu Tyr Ser Tyr Thr Gly Gln
230 235 240

Ser Ala Glu Glu Leu Ser Phe Pro Glu Gly Ala Leu Ile Arg Leu
245 250 255

Leu Pro Arg Ala Gln Asp Gly Val Asp Asp Gly Phe Trp Arg Gly
260 265 270

Glu Phe Gly Gly Arg Val Gly Val Phe Pro Ser Leu Leu Val Glu
275 280 285

Glu Leu Leu Gly Pro Pro Gly Pro Pro Glu Leu Ser Asp Pro Glu
290 295 300

Gln Met Leu Pro Ser Pro Ser Pro Pro Ser Phe Ser Pro Pro Ala

305	310	315
Pro Thr Ser Val Leu Asp Gly Pro Pro Ala Pro Val Leu Pro Gly		
320	325	330
Asp Lys Ala Leu Asp Phe Pro Gly Phe Leu Asp Met Met Ala Pro		
335	340	345
Arg Leu Arg Pro Met Arg Pro Pro Pro Pro Pro Pro Ala Lys Ala		
350	355	360
Pro Asp Pro Gly His Pro Asp Pro Leu Thr		
365	370	

<210> 316
 <211> 4407
 <212> DNA
 <213> Homo sapiens

<400> 316
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 agacacaggc agggagagac aaagatccag gaaaggaggg ctcaggagga 200
 gagtttgag aagccagacc cctgggcacc tctccaagc ccaaggacta 250
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aaggaaa 4407

<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

Met Ser Gln Thr Gly Ser His Pro Gly Arg Gly Leu Ala Gly Arg

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Trp Leu Trp Gly Ala Gln Pro Cys Leu Leu Leu Pro Ile Val Pro

20 25 30

Leu Ser Trp Leu Val Trp Leu Leu Leu Leu Leu Ala Ser Leu

35 40 45

Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu

50 55 60

Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser

65 70 75

Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu
80 85 90

Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu
95 100 105

Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly
110 115 120

Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp
125 130 135

Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu
140 145 150

Gly Val Leu Gln Tyr Arg Gly Ala Glu Leu His Leu Gln Pro Leu
155 160 165

Glu Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro Gly Ala His Ile
170 175 180

Leu Arg Arg Lys Ser Pro Ala Ser Gly Gln Gly Pro Met Cys Asn
185 190 195

Val Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg Arg Ala
200 205 210

Lys Arg Phe Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val Val
215 220 225

Ala Asp Asp Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg
230 235 240

Tyr Leu Leu Thr Val Met Ala Ala Ala Ala Lys Ala Phe Lys His
245 250 255

Pro Ser Ile Arg Asn Pro Val Ser Leu Val Val Thr Arg Leu Val
260 265 270

Ile Leu Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala
275 280 285

Ala Gln Thr Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn

290	295	300
Thr Pro Glu Asp Ser Gly Pro Asp His Phe Asp Thr Ala Ile Leu		
305	310	315
Phe Thr Arg Gln Asp Leu Cys Gly Val Ser Thr Cys Asp Thr Leu		
320	325	330
Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ala Arg Ser Cys		
335	340	345
Ala Ile Val Glu Asp Asp Gly Leu Gln Ser Ala Phe Thr Ala Ala		
350	355	360
His Glu Leu Gly His Val Phe Asn Met Leu His Asp Asn Ser Lys		
365	370	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu Ser Thr Ser Arg His Val		
380	385	390
Met Ala Pro Val Met Ala His Val Asp Pro Glu Glu Pro Trp Ser		
395	400	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu Asp Asn Gly Tyr		
410	415	420
Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu His Leu Pro		
425	430	435
Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln		
440	445	450
Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro		
455	460	465
Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala		
470	475	480
Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys		
485	490	495
Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp		
500	505	510

Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro
515 520 525

Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val
530 535 540

Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly
545 550 555

Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn
560 565 570

Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu
575 580 585

Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe
590 595 600

Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro
605 610 615

Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr
620 625 630

Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser
635 640 645

Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala
650 655 660

Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys
665 670 675

Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly
680 685 690

Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile
695 700 705

Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro
710 715 720

Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser

725	730	735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp		
740	745	750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr		
755	760	765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro		
770	775	780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg		
785	790	795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro		
800	805	810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu		
815	820	825
Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys		
830	835	

<210> 318

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

ccctgaagct gccagatggc tcc 23

<210> 319

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctgtgctctt cggcgcagcc agtc 24

<210> 320

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321

<211> 1197

<212> DNA

<213> Homo sapiens

<400> 321

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ttgtggactg gtgtttgta tcttggccct aactctaatt gtctgtttt 200

gggggagcaa gcacttctgg ccggaggtag ccaaaaaagc ctatgacatg 250

gagcacattt tctacagcaa tggagagaag aagaagattt acatggaaat 300

tgatcctgtg accagaactg aaatattcag aagcggaaat ggcactgatg 350

aaacattgga agtgcacgac tttaaaaacg gataactgg catctacttc 400

gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450

atcttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500

ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550

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<210> 322

<211> 317

<212> PRT

<213> Homo sapiens

<400> 322

Met Ala Lys Asn Pro Pro Glu Asn Cys Glu Asp Cys His Ile Leu

1 5 10 15

Asn Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys

20 25 30

Ile Cys Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val

35 40 45

Leu Phe Trp Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys

50 55 60

Ala Tyr Asp Met Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys

65	70	75
Lys Ile Tyr Met Glu Ile Asp Pro Val Thr Arg Thr Glu Ile Phe		
80	85	90
Arg Ser Gly Asn Gly Thr Asp Glu Thr Leu Glu Val His Asp Phe		
95	100	105
Lys Asn Gly Tyr Thr Gly Ile Tyr Phe Val Gly Leu Gln Lys Cys		
110	115	120
Phe Ile Lys Thr Gln Ile Lys Val Ile Pro Glu Phe Ser Glu Pro		
125	130	135
Glu Glu Glu Ile Asp Glu Asn Glu Glu Ile Thr Thr Thr Phe Phe		
140	145	150
Glu Gln Ser Val Ile Trp Val Pro Ala Glu Lys Pro Ile Glu Asn		
155	160	165
Arg Asp Phe Leu Lys Asn Ser Lys Ile Leu Glu Ile Cys Asp Asn		
170	175	180
Val Thr Met Tyr Trp Ile Asn Pro Thr Leu Ile Ser Val Ser Glu		
185	190	195
Leu Gln Asp Phe Glu Glu Glu Gly Glu Asp Leu His Phe Pro Ala		
200	205	210
Asn Glu Lys Lys Gly Ile Glu Gln Asn Glu Gln Trp Val Val Pro		
215	220	225
Gln Val Lys Val Glu Lys Thr Arg His Ala Arg Gln Ala Ser Glu		
230	235	240
Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile Glu Phe		
245	250	255
Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys Arg		
260	265	270
Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly		
275	280	285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
290 295 300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
305 310 315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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ggccgtgcag cttctgggct tcctgctcag ctctctgggc atggtgggca 150

cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtgggc 200

accaacatcc tcacggccgt gtctacctg aaagggctct ggatggagtg 250

tgtgtggcac agcacaggca tctaccagt ccagatctac cgatccctgc 300

tggcgctgcc ccaagacctc caggctgccc gcgcctcat ggtcatctcc 350

tgctgtctct cgggcatagc ctgcgcctgc gccgtcatcg ggatgaagtg 400

cacgcgtgc gccaaaggga caccgcgcaa gaccacctt gccatcctcg 450

gcggcaccct cttcatcctg gccggcctcc tgtgcatggt ggccgtctcc 500

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 ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324

<211> 239

<212> PRT

<213> Homo sapiens

<400> 324

Met Ala Ser Thr Ala Val Gln Leu Leu Gly Phe Leu Leu Ser Phe

1 5 10 15

Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp

20 25 30

Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser

35 40 45

Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly

50 55 60

Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln

65 70 75

Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu

80 85 90

Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr
95 100 105

Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu
110 115 120

Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala
125 130 135

Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro
140 145 150

Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr
155 160 165

Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu
170 175 180

Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln
185 190 195

Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala
200 205 210

Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val
215 220 225

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
230 235

<210> 325

<211> 2121

<212> DNA

<213> Homo sapiens

<400> 325

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cacatgcaa gtggtggcgt tcctcctgtc catcctgggg ctggccgget 150

gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac 200

aaccccgta cctccgtgtt ccagtagaa gggctctgga ggagctgcgt 250
gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300
gacttcagc catgctgcag gcagtgcgag ccctgatgat cgtaggcac 350
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ccgcattggc agcatggagg actctgcaa agccaacatg aactgacct 450
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gtacaccggc atgggtggga tggtcagac tgttcagacc aggtacacat 600
ttggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650
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<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

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Leu Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp
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Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln
35 40 45

Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe
50 55 60

Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met
65 70 75

Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly
80 85 90

Ala Ile Gly Leu Leu Val Ser Ile Phe Ala Leu Lys Cys Ile Arg
95 100 105

Ile Gly Ser Met Glu Asp Ser Ala Lys Ala Asn Met Thr Leu Thr
110 115 120

Ser Gly Ile Met Phe Ile Val Ser Gly Leu Cys Ala Ile Ala Gly
125 130 135

Val Ser Val Phe Ala Asn Met Leu Val Thr Asn Phe Trp Met Ser
140 145 150

Thr Ala Asn Met Tyr Thr Gly Met Gly Gly Met Val Gln Thr Val
155 160 165

Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe Val Gly Trp Val
170 175 180

Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met Cys Ile Ala
185 190 195

Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala Val Ser
200 205 210

Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly Phe
215 220 225

Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile

230 235 240
 Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro
 245 250 255
 Ser Lys His Asp Tyr Val
 260

<210> 327
 <211> 2010
 <212> DNA
 <213> Homo sapiens

<400> 327
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<210> 328

<211> 225

<212> PRT

<213> Homo sapiens

<400> 328

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Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp
20 25 30

Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn
35 40 45

Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile
50 55 60

Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro
65 70 75

Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met
80 85 90

Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr
95 100 105

Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu
110 115 120

Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile
125 130 135

Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn
140 145 150

Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu
155 160 165

Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala
170 175 180

Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr
185 190 195

Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
200 205 210

Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val
215 220 225

<210> 329

<211> 1315

<212> DNA

<213> Homo sapiens

<400> 329

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ctgcacttgc cctctggggg ggtcccaggg cccagccat tacatggccc 600
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<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

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Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
	20			25				30						

Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val
35 40 45

Val Trp Glu Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly
50 55 60

Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln
65 70 75

Asp Leu Gln Ala Ala Arg Ala Leu Cys Val Ile Ala Leu Leu Val
80 85 90

Ala Leu Phe Gly Leu Leu Val Tyr Leu Ala Gly Ala Lys Cys Thr
95 100 105

Thr Cys Val Glu Glu Lys Asp Ser Lys Ala Arg Leu Val Leu Thr
110 115 120

Ser Gly Ile Val Phe Val Ile Ser Gly Val Leu Thr Leu Ile Pro
125 130 135

Val Cys Trp Thr Ala His Ala Ile Ile Arg Asp Phe Tyr Asn Pro
140 145 150

Leu Val Ala Glu Ala Gln Lys Arg Glu Leu Gly Ala Ser Leu Tyr
155 160 165

Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu Gly Gly Gly Leu
170 175 180

Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly Pro Ser His
185 190 195

Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser Arg Gly
200 205 210

Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val
215 220

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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caagtgtaga atgattggact acttattact ttttgacat catgtattat 1100

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acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

1 5 10 15

Tyr Ser Ser Leu Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg

20 25 30

Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu

35 40 45

Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn

50 55 60

Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe

65 70 75

Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala

80 85 90

Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly

95 100 105

Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser

110 115 120

Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys

125 130 135

Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly

140 145 150

Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu

155

160

165

Ser Lys Thr Ser Thr Ser Tyr Val

170

<210> 333

<211> 535

<212> DNA

<213> Homo sapiens

<400> 333

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ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150

agaagtatcc agtgggtggcc atcccctgcc ccatcacata cctaccagtt 200

tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250

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ggtggggggac agagccagat tcagagtaat cttgactgaa tggagaaaagt 450

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<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

Met Lys Ile Thr Gly Gly Leu Leu Leu Cys Thr Val Val Tyr

1

5

10

15

Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val

20	25	30
Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys		
35	40	45
Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr		
50	55	60
Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly		
65	70	75
Arg Val Gln Phe Leu His Asp Gly Ser Cys		
80	85	

<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

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<210> 336

<211> 148

<212> PRT

<213> Homo sapiens

<400> 336

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20 25 30

Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val

35 40 45

Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu

50 55 60

Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg

65 70 75

Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met

80 85 90

Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu

95 100 105

Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln

110 115 120

Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr

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Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr

140 145

<210> 337

<211> 1310

<212> DNA

<213> Homo sapiens

<400> 337

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<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

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	20			25				30						

Thr	His	Thr	Ala	Glu	Gly	Gly	Asp	Pro	Leu	Pro	Gln	Pro	Ser	Gly
	35			40				45						

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp
	50			55				60						

Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg
	65			70				75						

His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr
	80			85				90						

Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu
	95			100				105						

Arg Leu Lys Phe Leu Asn Asp Ser Glu Gln Val Ala Arg Ala Trp
110 115 120

Pro His Asp Thr Ile Gly Ser Leu Lys Arg Thr Gln Phe Pro Gly
125 130 135

Arg Glu Gln Gln Val Arg Leu Ile Tyr Gln Gly Gln Leu Leu Gly
140 145 150

Asp Asp Thr Gln Thr Leu Gly Ser Leu His Leu Pro Pro Asn Cys
155 160 165

Val Leu His Cys His Val Ser Thr Arg Val Gly Pro Pro Asn Pro
170 175 180

Pro Cys Pro Pro Gly Ser Glu Pro Gly Pro Ser Gly Leu Glu Ile
185 190 195

Gly Ser Leu Leu Leu Pro Leu Leu Leu Leu Leu Leu Leu Leu
200 205 210

Trp Tyr Cys Gln Ile Gln Tyr Arg Pro Phe Phe Pro Leu Thr Ala
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230 235 240

Phe Ala Met Tyr Arg Pro
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<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

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ccttccatt tacaactaaa actgaccaga gcccaggaa taaatggtt 750

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tgttattgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met Thr Lys Ala Leu Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala

1 5 10 15

Leu Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val

20 25 30

Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser

35 40 45

Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser

50 55 60

Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe
65 70 75

Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser
80 85 90

Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn
95 100 105

Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala
110 115 120

Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly
125 130 135

Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg
140 145

<210> 341

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

ccctccaagg atgacaaagg cgc 23

<210> 342

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 342

ggtcagcagc tttcttgecc taaatcagg 29

<210> 343

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

atctcaggcg gcatcctgtc agcc 24

<210> 344

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

gtggatgcct gcaagaaggt tggg 24

<210> 345

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 345

agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346

<211> 2575

<212> DNA

<213> Homo sapiens

<400> 346

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caaaggggga aagaaacacc tgagcagaat ggaatcatta ttttttccc 150

aaggagaaaa ccggggtaaa gggaggggaag caattcaatt tgaagtcct 200

gtgaatgggc ttccagaagg caattaaaga aatccactca gagaggactt 250
gggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300
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tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met Leu Leu Arg Lys Arg Tyr Arg His Arg Pro Cys Arg Leu Gln

1 5 10 15

Phe Leu Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val

20 25 30

Ala Met Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr

35 40 45

Ala Gln Ala Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp

50 55 60

Phe Gly Glu Ser Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly

65 70 75

Glu Glu Tyr Ser Pro Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu

80 85 90

Arg Glu Asp Gln Leu Leu Val Ala Val Ala Leu Pro Gln Ala Arg

95 100 105

Arg Asn Gln Ser Gln Gly Arg Arg Gly Gly Ser Tyr Arg Leu Ile

110 115 120

Lys Gln Pro Arg Arg Gln Asp Lys Glu Ala Pro Lys Arg Asp Trp

125 130 135

Gly Ala Asp Glu Asp Gly Glu Val Ser Glu Glu Glu Glu Leu Thr

140 145 150

Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln Glu Ala Leu Ser Ala
155 160 165

Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val Arg His Pro Leu
170 175 180

Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr Ala Ser Val
185 190 195

Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu Arg Thr
200 205 210

Val His Ser Ile Leu Asp Thr Val Pro Arg Ala Phe Leu Lys Glu
215 220 225

Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser
230 235 240

Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Lys Leu Leu
245 250 255

Arg Ser Asn Lys Arg Leu Gly Ala Ile Arg Ala Arg Met Leu Gly
260 265 270

Ala Thr Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His
275 280 285

Cys Glu Cys His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile
290 295 300

Ala Gly Asp Arg Ser Arg Val Val Ser Pro Val Ile Asp Val Ile
305 310 315

Asp Trp Lys Thr Phe Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg
320 325 330

Gly Val Leu Asp Trp Lys Leu Asp Phe His Trp Glu Pro Leu Pro
335 340 345

Glu His Val Arg Lys Ala Leu Gln Ser Pro Ile Ser Pro Ile Arg
350 355 360

Ser Pro Val Val Pro Gly Glu Val Val Ala Met Asp Arg His Tyr

365	370	375
Phe Gln Asn Thr Gly Ala Tyr Asp Ser Leu Met Ser Leu Arg Gly		
380	385	390
Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala Trp Leu Cys Gly Gly		
395	400	405
Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly His Ile Tyr Gln		
410	415	420
Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala Thr Leu Arg		
425	430	435
Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe Lys Glu		
440	445	450
Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys Ala		
455	460	465
Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu		
470	475	480
Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu		
485	490	495
Leu Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His		
500	505	510
Asn Thr Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp		
515	520	525
Ile Leu Gly Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg		
530	535	540
Gln Gln Gln Tyr Leu Gln His Thr Ser Arg Lys Glu Ile His Phe		
545	550	555
Gly Ser Pro Gln His Leu Cys Phe Ala Val Arg Gln Glu Gln Val		
560	565	570
Ile Leu Gln Asn Cys Thr Glu Glu Gly Leu Ala Ile His Gln Gln		
575	580	585

His Trp Asp Phe Gln Glu Asn Gly Met Ile Val His Ile Leu Ser
590 595 600

Gly Lys Cys Met Glu Ala Val Val Gln Glu Asn Asn Lys Asp Leu
605 610 615

Tyr Leu Arg Pro Cys Asp Gly Lys Ala Arg Gln Gln Trp Arg Phe
620 625 630

Asp Gln Ile Asn Ala Val Asp Glu Arg
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<210> 348

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 348

ggagaggtgg tggccatgga cag 23

<210> 349

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 349

ctgtcactgc aaggagccaa cacc 24

<210> 350

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 350

tatgtcgtg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351

<211> 2524

<212> DNA

<213> Homo sapiens

<400> 351

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tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150

tcttcatcct cccctcgaac cccaccagcc ccagcccgcc ccccggtgctg 200

caggggaggc cctcggccc cacgtcatgt gtgcgtgtgg gagcgagcac 250

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tcaaataaag cctttgcaag ataa 2524

<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly

1 5 10 15

Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala

20 25 30

Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg

35 40 45

Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala

50 55 60

Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro

65 70 75

Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90

Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
95 100 105

Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
110 115 120

Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
140 145 150

Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
155 160 165

Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
170 175 180

Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
185 190 195

Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
200 205 210

Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
215 220 225

Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
230 235 240

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

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<210> 354

<211> 121

<212> PRT

<213> Homo sapiens

<400> 354

Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser

1 5 10 15

Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu

20 25 30

Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly

35 40 45

Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp

50 55 60

Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser

65 70 75

Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro

80 85 90

Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys

95 100 105

Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala
110 115 120

Ser

<210> 355

<211> 2134

<212> DNA

<213> Homo sapiens

<400> 355

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gtgcctgacg gcggcgctgg cccacggctg tctgactgc cacagcaact 150

tctccaagaa gttctccttc taccgccacc atgtgaactt caagtcttg 200

tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250

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agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350

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catcttcgg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450

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tggcatcttc cagtacgaga ccattcctg caacaactgc acagactgc 750

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<210> 356

<211> 157

<212> PRT

<213> Homo sapiens

<400> 356

Met Ala Leu Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala
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His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser
 20 25 30

Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp
 35 40 45

Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr
 50 55 60

Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu
 65 70 75

Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln
 80 85 90

Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu
 95 100 105

Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala
 110 115 120

Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln

125	130	135
Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro		
140	145	150
Ser Pro Arg Gly Asp Leu Pro		
155		

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

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acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200

cataggcttc ttccaggatt tagaaatacc agcagtgtccc atactccata 250

gcatggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300

gaggttctga cacactacaa catcactggg aacaccatct gcctctttcg 350

cctggtagac aatgaacaac tgaattaga ggacgaagac attgaaagca 400

ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450

gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500

tcagattcat ctctctctga taatgaacaa ggcctcccca gagtatgaag 550

agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600

ctctttattc tgggtggacag tggatatgaa gaaaatggga aggtgatatc 650

atthttcaaa ctaaaggagt ctcaactgcc agctttggca atttaccaga 700

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<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

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Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser
		20		25				30						

Ser Asp Gly Pro Gly Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp
35 40 45

Val Pro Ala Ala Met Glu Phe Ile Ala Ala Thr Glu Val Ala Val
50 55 60

Ile Gly Phe Phe Gln Asp Leu Glu Ile Pro Ala Val Pro Ile Leu
65 70 75

His Ser Met Val Gln Lys Phe Pro Gly Val Ser Phe Gly Ile Ser
80 85 90

Thr Asp Ser Glu Val Leu Thr His Tyr Asn Ile Thr Gly Asn Thr
95 100 105

Ile Cys Leu Phe Arg Leu Val Asp Asn Glu Gln Leu Asn Leu Glu
110 115 120

Asp Glu Asp Ile Glu Ser Ile Asp Ala Thr Lys Leu Ser Arg Phe
125 130 135

Ile Glu Ile Asn Ser Leu His Met Val Thr Glu Tyr Asn Pro Val
140 145 150

Thr Val Ile Gly Leu Phe Asn Ser Val Ile Gln Ile His Leu Leu
155 160 165

Leu Ile Met Asn Lys Ala Ser Pro Glu Tyr Glu Glu Asn Met His
170 175 180

Arg Tyr Gln Lys Ala Ala Lys Leu Phe Gln Gly Lys Ile Leu Phe
185 190 195

Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val Ile Ser
200 205 210

Phe Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile Tyr
215 220 225

Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val
230 235 240

Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe Leu Ser Gly

245 250 255

Lys Leu Leu Lys Glu Asn Arg Glu Ser Glu Gly Lys Thr Pro Lys
260 265 270

Val Glu Leu

<210> 359

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 359

ccagcagtgc ccatactcca tagc 24

<210> 360

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 360

tgacgagtgg gatacactgc 20

<210> 361

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 361

gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 362

attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363

<211> 1777

<212> DNA

<213> Homo sapiens

<400> 363

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ccggcgcggg tggcggagag atcagaagcc tcttcccaa gccgagcaa 100

cctcagcggg gacccgggct caggacgcg gcggcggcgg cggcgactgc 150

agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200

cccagacagc cggcgtggc tgtgtcggt gctggcggcg gcgcttgggc 250

tcttgacagc tggagtatca gccttggaag tatatacgcc aaaagaaatc 300

tctgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350

tagtacgact ggcgggtga cctcagtctc ctggagcttc cagccagagg 400

gggccgacac tactgtgtcg ttttccact actcccaagg gcaagtgtac 450

cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500

tgacaagaaa gatgcatcaa tcaacataga aaatatgcag ttatacaca 550

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cgtggagagt aaaaagtatc ggtttta 1777

<210> 364

<211> 269

<212> PRT

<213> Homo sapiens

<400> 364

Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp

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Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu

20 25 30

Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu

35 40 45

Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe

50 55 60

Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser

65 70 75

Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr

80 85 90

Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp

95 100 105

Arg Ile Ser Trp Ala Gly Asp Leu Asp Lys Lys Asp Ala Ser Ile

110 115 120

Asn Ile Glu Asn Met Gln Phe Ile His Asn Gly Thr Tyr Ile Cys

125 130 135

Asp Val Lys Asn Pro Pro Asp Ile Val Val Gln Pro Gly His Ile

140 145 150

Arg Leu Tyr Val Val Glu Lys Glu Asn Leu Pro Val Phe Pro Val

155 160 165

Trp Val Val Val Gly Ile Val Thr Ala Val Val Leu Gly Leu Thr

170 175 180

Leu Leu Ile Ser Met Ile Leu Ala Val Leu Tyr Arg Arg Lys Asn

185	190	195
Ser Lys Arg Asp Tyr Thr Gly Cys Ser Thr Ser Glu Ser Leu Ser		
200	205	210
Pro Val Lys Gln Ala Pro Arg Lys Ser Pro Ser Asp Thr Glu Gly		
215	220	225
Leu Val Lys Ser Leu Pro Ser Gly Ser His Gln Gly Pro Val Ile		
230	235	240
Tyr Ala Gln Leu Asp His Ser Gly Gly His His Ser Asp Lys Ile		
245	250	255
Asn Lys Ser Glu Ser Val Val Tyr Ala Asp Ile Arg Lys Asn		
260	265	

<210> 365

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 365

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tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
aggggcgcgg ccccggcgca gtccccgcg gccccgacc ctgaggcgtc 250
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<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro

1

5

10

15

Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg
20 25 30

Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly
35 40 45

Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu
50 55 60

Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu
65 70 75

Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro
80 85 90

Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala
95 100 105

Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp
110 115 120

Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly
125 130 135

Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn
140 145 150

Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile
155 160 165

Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala
170 175 180

Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu
185 190 195

Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr
200 205 210

Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys
215 220 225

Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys

230	235	240
Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys		
245	250	255
Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu		
260	265	270
Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn		
275	280	285
Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn		
290	295	300
Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe		
305	310	315
Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu		
320	325	330
Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp		
335	340	345
Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val		
350	355	360
Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg		
365	370	

<210> 367

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 367

tggaagaa gtctggtcag aaggttagg 30

<210> 368

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 368

catttgctt cattctctg ctctg 25

<210> 369

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 369

aaaacctcag aacaactcat ttgcacc 28

<210> 370

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 370

gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371

<211> 1150

<212> DNA

<213> Homo sapiens

<400> 371

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gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100

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<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met Ala Ala Ser Ala Gly Ala Thr Arg Leu Leu Leu Leu Leu
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Leu Met Ala Val Ala Ala Pro Ser Arg Ala Arg Gly Ser Gly Cys
20 25 30

Arg Ala Gly Thr Gly Ala Arg Gly Ala Gly Ala Glu Gly Arg Glu
35 40 45

Gly Glu Ala Cys Gly Thr Val Gly Leu Leu Leu Glu His Ser Phe
50 55 60

Glu Ile Asp Asp Ser Ala Asn Phe Arg Lys Arg Gly Ser Leu Leu
65 70 75

Trp Asn Gln Gln Asp Gly Thr Leu Ser Leu Ser Gln Arg Gln Leu
80 85 90

Ser Glu Glu Glu Arg Gly Arg Leu Arg Asp Val Ala Ala Leu Asn
95 100 105

Gly Leu Tyr Arg Val Arg Ile Pro Arg Arg Pro Gly Ala Leu Asp
110 115 120

Gly Leu Glu Ala Gly Gly Tyr Val Ser Ser Phe Val Pro Ala Cys
125 130 135

Ser Leu Val Glu Ser His Leu Ser Asp Gln Leu Thr Leu His Val
140 145 150

Asp Val Ala Gly Asn Val Val Gly Val Ser Val Val Thr His Pro
155 160 165

Gly Gly Cys Arg Gly His Glu Val Glu Asp Val Asp Leu Glu Leu
170 175 180

Phe Asn Thr Ser Val Gln Leu Gln Pro Pro Thr Thr Ala Pro Gly
185 190 195

Pro Glu Thr Ala Ala Phe Ile Glu Arg Leu Glu Met Glu Gln Ala
200 205 210

Gln Lys Ala Lys Asn Pro Gln Glu Gln Lys Ser Phe Phe Ala Lys
215 220 225

Tyr Trp Met Tyr Ile Ile Pro Val Val Leu Phe Leu Met Met Ser
230 235 240

Gly Ala Pro Asp Thr Gly Gly Gln Gly Gly Gly Gly Gly Gly
245 250 255

Gly Gly Gly Gly Ser Gly Leu Cys Cys Val Pro Pro Ser Leu
260 265

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

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ctggacttct atcaggctca ctctctggcc ctggcagctg attggcttca 300

ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350

aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400

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aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser
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Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly
20 25 30

Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe
35 40 45

Tyr Gln Val Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala
50 55 60

Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly
65 70 75

Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu
80 85 90

Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys
95 100 105

Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu
110 115 120

Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala
125 130 135

Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala
140 145 150

Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu
155 160 165

Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val
170 175 180

Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp

185	190	195
Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu		
200	205	210
Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu Asn		
215	220	225
Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu		
230	235	240
Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile		
245	250	255
Gln Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp		
260	265	270
Thr Pro Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe		
275	280	285
Ser Ser Phe Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg		
290	295	300
Ile Ala Thr Ser Lys Arg Tyr His Leu Gln Pro Met His Leu Leu		
305	310	315
Ser Leu Ala Val Leu Ile Val Val Phe Ser Leu Phe Met Leu Thr		
320	325	330
Phe Ser Thr Ser Pro Gly Gln Glu Ser Pro Val Glu Ser Phe Ile		
335	340	345
Ala Phe Leu Leu Ile Glu Leu Ala Cys Gly Leu Tyr Phe Pro Ser		
350	355	360
Met Ser Phe Leu Arg Arg Lys Val Ile Pro Glu Thr Glu Gln Ala		
365	370	375
Gly Val Leu Asn Trp Phe Arg Val Pro Leu His Ser Leu Ala Cys		
380	385	390
Leu Gly Leu Leu Val Leu His Asp Ser Asp Arg Lys Thr Gly Thr		
395	400	405

Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met Val Met Ala Leu
410 415 420

Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His Asp Ala Glu
425 430 435

Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro Glu Leu
440 445 450

<210> 375

<211> 1098

<212> DNA

<213> Homo sapiens

<400> 375

gcgacgcgcg gcggggcggc gagaggaaac gcggcgccgg gccgggcccg 50

gccctggaga tggccccgg cgccgcgggc tgggtgtgctc tcgtgctctg 100

gctccccgcg tgcgtcgcgg cccacggctt cegtatccat gattatttgt 150

actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200

cctgccaaagg actttggtgg tatctttcac acaaggtatg agcagattca 250

ccttgcccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300

tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350

ctctccaaga ctcggtgtgt ccaggagcac ggcgggcggg cggtgatcat 400

ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450

acagtaccca gcgcacagct gacatccccg cctcttctct gctcggccga 500

gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550

catcatttcc atcccagtc atgtcaccag catccccacc tttagctgc 600

tgcaaccgcc ctggaccttc tggtagaaga gttgtccca cattccagcc 650

ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700

aatttgaga tagcatctgg ggacaagtgg agccaggtag aggaaaagg 750
tttggcggtt gctaggctga aagggaagcc acaccactgg ccttccttc 800
cccagggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850
ccccagggct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900
gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
taccaggggt ctctgcacag tgaccttcac agcagttgtt ggagtgggtt 1000
aaagagctgg tgtttgggga ctcaataaac cctcactgac ttttagcaa 1050
taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu
1 5 10 15

Pro Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu
20 25 30

Tyr Phe Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr
35 40 45

Ala Thr Pro Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr
50 55 60

Glu Gln Ile His Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly
65 70 75

Glu Leu Ser Asn Gly Phe Phe Ile Gln Asp Gln Ile Ala Leu Val
80 85 90

Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln
95 100 105

Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp
110 115 120

Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg
125 130 135

Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr
140 145 150

Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile
155 160 165

Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu
170 175 180

Leu Gln Pro Pro Trp Thr Phe Trp
185

<210> 377

<211> 496

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 396

<223> unknown base

<400> 377

tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50

ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100

ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctctccta 150

ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200

atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250

aagacccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300

ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350

tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378

<211> 116

<212> PRT

<213> Homo sapiens

<400> 378

Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val Met Ala Gly Val

1 5 10 15

Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys

20 25 30

Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly

35 40 45

Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr

50 55 60

Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys

65 70 75

Thr Gln Gly Cys Gly Ile Tyr Lys Asp Asn Asn Lys Ser Ser Ile

80 85 90

His Cys Met Asp Leu Ser Gln Arg Tyr Cys Leu Met Ala Val Phe

95 100 105

Asn Val Ile Tyr Leu Glu Asn Glu Asp Ser Glu

110 115

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 379

ctgcctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

cagagcagtg gatgtcccc tggg 24

<210> 381

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 381

ctgaacaaga tggtaagca agtgactggg aaaatgcca tcctc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

ctcgtctt cttcttgat gggggcccag gggggccagg agagtataa 50

ggcgatgtg aggggtgccc gcacaaccag acgcccagtc acaggcgaga 100

gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150

ctcttggggg gcccacctg ggcagggaag atgtatggcc ctggaggagg 200

caagtatttc agcaccactg aagactacga ccatgaaatc acagggtgc 250

gggtgtctgt aggtcttctc ctggtgaaaa gtgtccagggt gaaacttga 300

gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350

caccctgcag ccaggcgaat acatcacaaa agtctttgtc gcctccaag 400

cttctctccg gggatatgtc atgtacacca gcaaggaccg ctatttctat 450

tttgggaagc ttgatggcca gatctcctct gcctacccca gccaaagagg 500

gcaggtgctg gtgggcatct atggccagta tcaactcctt ggcatcaaga 550

gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600

ccagttaatc tcacatactc agcaaactca cccgtgggtc gctagggtgg 650

ggatatggggc catccgagct gaggccatct gtgtgggtgt ggctgatgtt 700

actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750

gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu

1 5 10 15

Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly

20 25 30

Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr

35 40 45

Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln

50 55 60

Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly

65 70 75

Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr

80 85 90

Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met
95 100 105

Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly
110 115 120

Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val
125 130 135

Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly
140 145 150

Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro
155 160 165

Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg
170 175

<210> 384

<211> 2379

<212> DNA

<213> Homo sapiens

<400> 384

gctgagcgtg tgcgcggtac ggggctctcc tgccttctgg gctccaacgc 50

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atacagatgt ggcagctcag gtagccccaa attgcctgga agaatacatc 150

atgttttctg ataagaagaa attgtaggat ccagttttt tttaaccgc 200

cccccccca ccccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250

atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300

tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350

atgttccaaa atcgggccat ctccaagggt gtccaatttt tcttctggg 400

tgtcagcgag ccctgactca ctacagtgca gctgacagggt gctgtcatgc 450

aactggcccc taagccaaag caaaagacct aaggacgacc ttgaacaat 500

acaaaggatg gggttcaatg taattaggct actgagcggg tcagctgtag 550
cactgggtat agccccact gtcttactga caatgcttgc ttctgccgaa 600
cgaggatgcc ctaagggctg taggtgtgaa ggcaaatgg tatattgtga 650
atctcagaaa ttacaggaga taccctcaag tatactgtct ggttgcttag 700
gtttgtccct tcgtataac agccttcaaa aacttaagta taatcaattt 750
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caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850
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gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950
gggatctgaa cagtttcggg gcttgccgaa gctgctgagt ttacatttac 1000
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 ctcgtcatcc tgctggttat ctacgtgtca tggaagcggg accctgcgag 1850
 catgaagcag ctgcagcagc gctccctcat gcgaaggcac aggaaaaaga 1900
 aaagacagtc cctaaagcaa atgactocca gcaccagga attttatgta 1950
 gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000
 gggaccctgc acctataaca aatcgggctc caggagtggt gaggtatgaa 2050
 ccattgtgat aaaaagagct cttaaagct gggaaataag tggcgcttta 2100
 ttgaactctg gtgactatca agggaacgcg atgccccccc tcccctccc 2150
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 tcataatact ggtcatttc ctctcataca taatcaacc attgaaattt 2250
 aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300
 ttgtataaga ccccttactg attccattaa tgcgcattt gttttaagat 2350
 aaaacttctt tcataggtaa aaaaaaaaa 2379

<210> 385

<211> 513

<212> PRT

<213> Homo sapiens

<400> 385

Met Gly Phe Asn Val Ile Arg Leu Leu Ser Gly Ser Ala Val Ala

1 5 10 15

Leu Val Ile Ala Pro Thr Val Leu Leu Thr Met Leu Ser Ser Ala

20 25 30

Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val
35 40 45

Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser
50 55 60

Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys
65 70 75

Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu
80 85 90

Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe
95 100 105

Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg
110 115 120

Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu
125 130 135

Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser
140 145 150

Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg
155 160 165

Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys
170 175 180

Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser
185 190 195

Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu
200 205 210

His Leu Glu His Asn Gln Phe Ser Lys Leu Asn Leu Ala Leu Phe
215 220 225

Pro Arg Leu Val Ser Leu Gln Asn Leu Tyr Leu Gln Trp Asn Lys
230 235 240

Ile Ser Val Ile Gly Gln Thr Met Ser Trp Thr Trp Ser Ser Leu

245	250	255
Gln Arg Leu Asp Leu Ser Gly Asn Glu Ile Glu Ala Phe Ser Gly		
260	265	270
Pro Ser Val Phe Gln Cys Val Pro Asn Leu Gln Arg Leu Asn Leu		
275	280	285
Asp Ser Asn Lys Leu Thr Phe Ile Gly Gln Glu Ile Leu Asp Ser		
290	295	300
Trp Ile Ser Leu Asn Asp Ile Ser Leu Ala Gly Asn Ile Trp Glu		
305	310	315
Cys Ser Arg Asn Ile Cys Ser Leu Val Asn Trp Leu Lys Ser Phe		
320	325	330
Lys Gly Leu Arg Glu Asn Thr Ile Ile Cys Ala Ser Pro Lys Glu		
335	340	345
Leu Gln Gly Val Asn Val Ile Asp Ala Val Lys Asn Tyr Ser Ile		
350	355	360
Cys Gly Lys Ser Thr Thr Glu Arg Phe Asp Leu Ala Arg Ala Leu		
365	370	375
Pro Lys Pro Thr Phe Lys Pro Lys Leu Pro Arg Pro Lys His Glu		
380	385	390
Ser Lys Pro Pro Leu Pro Pro Thr Val Gly Ala Thr Glu Pro Gly		
395	400	405
Pro Glu Thr Asp Ala Asp Ala Glu His Ile Ser Phe His Lys Ile		
410	415	420
Ile Ala Gly Ser Val Ala Leu Phe Leu Ser Val Leu Val Ile Leu		
425	430	435
Leu Val Ile Tyr Val Ser Trp Lys Arg Tyr Pro Ala Ser Met Lys		
440	445	450
Gln Leu Gln Gln Arg Ser Leu Met Arg Arg His Arg Lys Lys Lys		
455	460	465

Arg Gln Ser Leu Lys Gln Met Thr Pro Ser Thr Gln Glu Phe Tyr
470 475 480

Val Asp Tyr Lys Pro Thr Asn Thr Glu Thr Ser Glu Met Leu Leu
485 490 495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
500 505 510

Cys Glu Val

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 386

ctgggatctg aacagtttcg gggc 24

<210> 387

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

ggtccccagg acatggtctg tccc 24

<210> 388

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 389

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ttgactgtcc tttaaatacg tcaagatcca gacttttcag tgtcacctca 100

gcgactctca cgaataggat cttgtgttg ccgctattcc agttggtgct 150

ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa tggtcggtat atctggatcc tctgctgct ggttttggtg 250

gcagctcttc tctgtggagc tgggtcttc tgcctccagt gctggctgag 300

gagaccccca attgattctc acaggcgcac catggcagtt ttgctgttg 350

gagacttgga ctctatttat gggacagaag cagctgtgag tccaactgtt 400

ggaattcacc ttcaaacctc aaccctgac ctatccttg ttctgctcc 450

atgttttggc cctttaggct cccacctcc atatgaagaa attgtaaaaa 500

caacctgatt ttagggtggtg attatcaatt taaagtatta acgacatctg 550

taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600

tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650

ggatgttgga aaaaattttg gtcattggaga tgtttaaata gtaaagtagc 700

aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750

attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800

gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850

tctgctttaa actcttctct agcatggggt ccataaaaat tattataatt 900

taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950
 agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000
 tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050
 gtctcagcaa aaacaagagg tttatgccc caacctgaag aggaagaaat 1100
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 ccaacacggg gagaaaagaa aatttccct ttacagtaa tgaatgtggc 1200
 ctccatagtc catagtgtt ctctggagcc tcagggttg gcatttattg 1250
 cagcatcatg ctaagaacct tcggcatagg tatctgttc catgaggact 1300
 gcagaagtag caatgagaca tctcaagtg gcatttggc agtggccatc 1350
 agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400
 ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met Ser Arg Ser Arg Leu Phe Ser Val Thr Ser Ala Ile Ser Thr

1 5 10 15

Ile Gly Ile Leu Cys Leu Pro Leu Phe Gln Leu Val Leu Ser Asp

20 25 30

Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln

35 40 45

His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Val Leu

50 55 60

Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys

65 70 75

Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala
80 85 90

Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala
95 100 105

Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro
110 115 120

Asp Leu Tyr Pro Val Pro Ala Pro Cys Phe Gly Pro Leu Gly Ser
125 130 135

Pro Pro Pro Tyr Glu Glu Ile Val Lys Thr Thr
140 145

<210> 391

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

cttttcagtg tcacctcagc gatctc 26

<210> 392

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

ccaaaacatg gagcaggaac agg 23

<210> 393

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 394

gagcggagta aaatctccac aagctgggaa caaacctcgt cccaactccc 50

accaccggc gtttctccag ctcatctgg aggtgcttc gccagtgtg 100

gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150

aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200

tcttctctac ttgggagag agagaaagtc agatgccctt tttaactcc 250

ctcttcaaaa ctcatctct gggtgactga gttaatagag tggatacaac 300

cttgctgaag atgaagaata tacaatattg aggatatatt tttcttttt 350

ttttcaagtc ttgattgtg gcttacctca agttaccatt tttcagtcaa 400

gtctgttgt ttgcttcitc agaaatgtt ttacaatct caagaaaaaa 450

tatgtccag aaattgagtt tactgttgc tgtatttga ctcatttggg 500

gattgatgt actgcactat acttttcaac aaccaagaca tcaaagcagt 550

gtcaagttac gtgagcaaat actagactta agcaaaagat atgttaaagc 600

tctagcagag gaaaataaga acacagtgga tctcgagaac ggtgcttcta 650

tggcaggata tgcggatctg aaaagaacaa ttgctgtcct tctggatgac 700

attttgaac gattggtgaa gctggagaac aaagttgact atattgttgt 750

gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttggtgc 800

cagtaaccac aaataaaaga acgaatgtct cgggcagtat cagatagcag 850

ttgaaaatca ccttgtgctg ctccatccac tgtggattat atcctatggc 900

agaaaagctt tataattgct ggcttaggac agagcaatac ttacaataa 950

aagctctaca catttcaag gagtatgctg gattcatgga actctaattc 1000

tgtacataaa aattttaag ttattgttt gcttcaggc aagtctgttc 1050

aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggt 1100

aagcagatag gtgagttttg tataaatctt ttgtgttga gatcaagctg 1150

aaatgaaaac actgaaaaac atggattcat ttctataaca catttattta 1200

agtatataac acgtttttg gacaagtga gaagtgttaa tcattctgtc 1250

attgttctc aatagatgta actgttagac tacggctatt tgaaaaaatg 1300

tgcttattgt actatatttt gttattccaa ttatgagcag agaaaggaaa 1350

tataatgttg aaaataatgt ttgaaatca tgacccaaag aatgtattga 1400

tttgactat ccttcagaat aactgaaggt taattattgt atattttta 1450

aaattacact tataagagta taatcttgaa atgggttagca gccactgtcc 1500

attacctatc gtaaacattg gggcaattta ataacagcat taaaatagtt 1550

gtaaactcta atcttatact tattgaagaa taaaagatat ttttatgatg 1600

agagtaacaa taaagtattc atgattttc acatacatga atgttcattt 1650

aaaagttaa tcctttgagt gtctatgcta tcaggaaagc acattatttc 1700

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tttgagaat ggaactcttg aggactttag ccagggtgat ataataaagg 1800

tacttttgtg ctgcattaaa ttgcttgga agtgtaaca ttatattata 1850

taagagtatc ctttatgaaa ttttgaattt gtataacaga tgcattagat 1900

attcatttta tataatggcc acttaaaata agaacattta aaatataaac 1950
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 catgtagcaa taattacaat attttattaa aataaatatg tgaaatattg 2250
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 acctttatgt gaagaaatta attatatgcc attgccaggt 2340

<210> 395
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 395
 Met Phe Phe Thr Ile Ser Arg Lys Asn Met Ser Gln Lys Leu Ser
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 Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu
 20 25 30
 His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu
 35 40 45
 Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu
 50 55 60
 Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser
 65 70 75
 Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu
 80 85 90
 Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp

95	100	105
Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr		
110	115	120
Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val		
125	130	135
Ser Gly Ser Ile Arg		
140		

<210> 396

<211> 2639

<212> DNA

<213> Homo sapiens

<400> 396

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acctgggcc ttctgacag ctccagcctg actcgggtgg attgtagcgg 200

cctgggcccc cacatcatgc cgtgcccac cctctggac acagcccact 250

tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttgcg 300

gggcccgggt acacgacgtt ggctggcctg gatctcagcc acaacctgct 350

caccagcatc tcaccactg ccttctccc ccttcgctac ctggagtcgc 400

ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450

agctcacccc tgagcgacgt gaaccttagc cacaaccagc tccgggaggt 500

ctcagtgtct gccttcacga cgcacagtca gggccgggca ctacagtgg 550

accttccca caacctcatt caccgcctg tgccccacc cagagggcc 600

ggcctgcctg cgcccacat tcagagcctg aacctggcct ggaaccggct 650

ccatgccgtg cccaacctcc gagacttgcc cctgcgctac ctgagcctgg 700
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397

<211> 353

<212> PRT

<213> Homo sapiens

<400> 397

Met Pro Trp Pro Leu Leu Leu Leu Leu Ala Val Ser Gly Ala Gln

1	5	10	15
Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr			
20	25	30	
Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser			
35	40	45	
Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr			
50	55	60	
Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu			
65	70	75	
Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp			
80	85	90	
Leu Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser			
95	100	105	
Arg Leu Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu			
110	115	120	
Thr Ala Leu Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp			
125	130	135	
Val Asn Leu Ser His Asn Gln Leu Arg Glu Val Ser Val Ser Ala			
140	145	150	
Phe Thr Thr His Ser Gln Gly Arg Ala Leu His Val Asp Leu Ser			
155	160	165	
His Asn Leu Ile His Arg Leu Val Pro His Pro Thr Arg Ala Gly			
170	175	180	
Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala Trp Asn Arg			
185	190	195	
Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg Tyr Leu			
200	205	210	
Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala Phe			
215	220	225	

Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln
230 235 240

Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly
245 250 255

Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala
260 265 270

Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp
275 280 285

Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu
290 295 300

His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg
305 310 315

Cys Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly
320 325 330

Ser Ser Pro Lys Val Pro Leu His Cys Val Asp Thr Arg Glu Ser
335 340 345

Ala Ala Arg Gly Pro Thr Ile Leu
350

<210> 398

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

ccctgccagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 400

caacccaag cttaactggg caggagctga ggtgtttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatggcgag ccacagcttc tgtgagattc gatttctccc cagtccct 50

gtgggtctga ggggaccaga agggtagct acgttggtt tctggaagg 100

gaggctatat gcgtcaattc cccaaaaca gtttgacat tccccctgaa 150

atgcattct ctatctattc actgcaagt cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

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ccaattcctt tcttaccatc aagaaggacc tccggctctc tcatgccac 750

atgacatgcc attgtgggga ggaagcaatg aagaaataca gccagattct 800

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gggaactaga cattctctg caatggatgg aggagacaga ataggaggaa 900

agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950

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ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500

aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550

ccaaaaaaaa aaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

Met Arg Gln Phe Pro Lys Thr Ser Phe Asp Ile Ser Pro Glu Met
1 5 10 15

Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu
20 25 30

Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys
35 40 45

Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu
50 55 60

Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu
65 70 75

Leu Leu Trp Ser Pro Asp Phe Arg Pro Lys Met Lys Ala Ser Ser
80 85 90

Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr Leu Leu Trp Thr
95 100 105

Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser Cys Val Ile
110 115 120

Ala Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Glu Ile Arg
125 130 135

Gly Ser Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile Leu
140 145 150

Arg Arg Thr Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys
155 160 165

Cys Leu Leu Arg His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe
170 175 180

Lys Asn Tyr Gln Thr Pro Asp His Tyr Thr Leu Arg Lys Ile Ser

185	190	195
Ser Leu Ala Asn Ser Phe Leu Thr Ile Lys Lys Asp Leu Arg Leu		
200	205	210
Ser His Ala His Met Thr Cys His Cys Gly Glu Glu Ala Met Lys		
215	220	225
Lys Tyr Ser Gln Ile Leu Ser His Phe Glu Lys Leu Glu Pro Gln		
230	235	240
Ala Ala Val Val Lys Ala Leu Gly Glu Leu Asp Ile Leu Leu Gln		
245	250	255
Trp Met Glu Glu Thr Glu		
260		

<210> 403

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

ctcctgtggt ctccagattt caggccta 28

<210> 404

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 404

agtcctcctt aagattctga tgtcaa 26

<210> 405

<211> 998

<212> DNA

<213> Homo sapiens

<400> 405

ccgttatcgt cttgcgctac tgctgaatgt ccgtcccga ggaggaggag 50
aggcttttgc cgctgacca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggtaccg tggccgagct agcaaccttt cccctggatc 150
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cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406

<211> 323

<212> PRT

<213> Homo sapiens

<400> 406

Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln

1 5 10 15

Arg Trp Pro Arg Ala Ser Lys Phe Leu Leu Ser Gly Cys Ala Ala

20 25 30

Thr Val Ala Glu Leu Ala Thr Phe Pro Leu Asp Leu Thr Lys Thr

35 40 45

Arg Leu Gln Met Gln Gly Glu Ala Ala Leu Ala Arg Leu Gly Asp

50 55 60

Gly Ala Arg Glu Ser Ala Pro Tyr Arg Gly Met Val Arg Thr Ala

65 70 75

Leu Gly Ile Ile Glu Glu Glu Gly Phe Leu Lys Leu Trp Gln Gly

80 85 90

Val Thr Pro Ala Ile Tyr Arg His Val Val Tyr Ser Gly Gly Arg

95 100 105

Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly Lys Ser

110 115 120

Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly Met

125 130 135

Met Ala Gly Val Ile Gly Gln Phe Leu Ala Asn Pro Thr Asp Leu

140 145 150

Val Lys Val Gln Met Gln Met Glu Gly Lys Arg Lys Leu Glu Gly

155 160 165

Lys Pro Leu Arg Phe Arg Gly Val His His Ala Phe Ala Lys Ile

170 175 180

Leu Ala Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly Trp Val Pro

185 190 195

Asn Ile Gln Arg Ala Ala Leu Val Asn Met Gly Asp Leu Thr Thr
200 205 210

Tyr Asp Thr Val Lys His Tyr Leu Val Leu Asn Thr Pro Leu Glu
215 220 225

Asp Asn Ile Met Thr His Gly Leu Ser Ser Leu Cys Ser Gly Leu
230 235 240

Val Ala Ser Ile Leu Gly Thr Pro Ala Asp Val Ile Lys Ser Arg
245 250 255

Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr
260 265 270

Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly
275 280 285

Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met
290 295 300

Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg
305 310 315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

cgcgatccc gttatcgtct tgcgctactg c 31

<210> 408

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

gcggaattct taaaatggac tgactccact catc 34

<210> 409

<211> 1487

<212> DNA

<213> Homo sapiens

<400> 409

cggacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50

tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100

cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150

tagataattt tcgttgcca gaatgtgaat gtattgactg gagtgagaga 200

agaaatgctg tggcatctgt tgcgcaggt atattgttt ttacaggctg 250

gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagtga 300

accatgccct tcacacatgt ggtgtatttt ccacattggc tttctcatg 350

ataaatgctg tatccaatgc tcaggtgaga ggtgatatct atgaaagcgg 400

ctgttttaga agaacaggtg ctcgagtttg gcttttcatt ggtttcatgt 450

tgatgtttgg gtcacttatt gcttccatgt ggattctttt tggatcatat 500

gttaccctaaa atactgatgt ttatccggga ctagctgtgt ttttcaaaa 550

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<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys

1 5 10 15

Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala

20 25 30

Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala

35 40 45

Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr
50 55 60

Cys Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val
65 70 75

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu
80 85 90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu
95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala
110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe
125 130 135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe
140 145 150

Gly Arg Thr Glu Glu Leu Trp Thr
155

<210> 411

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

gtttgaggaa gctgggatac 20

<210> 412

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

ccaaactcga gcacctgttc 20

<210> 413

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

atggcaggt tctagataa tttcgttg ccagaatgtg 40

<210> 414

<211> 1337

<212> DNA

<213> Homo sapiens

<400> 414

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gcagctggcc cactggcggc ccgaacact ccgtctcacc ctctgggccc 100

actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150

gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200

gggacctacg gcacctgctg gaccacctcg cttctccat cgaagcaggg 250

aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300

acctggacag gatgagagtg tcaggtgtgc ttgcctcct ggccctcacc 350

tttccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400

catgaaaacc atccgtctgc cacgttggtt ggcagcctcg cccaccaagg 450

agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500

aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtgggccc 550

tactatgtgc ttgaagacc gcatgatcat gagtctgtg aaaaacaatg 600

tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650
 ctgggacaga aggcatattga catgtactct ggagatgtta tgcacctagt 700
 gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctcct 750
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 accagctgtc tgtggagaga atggggtgct ttcgtcaggg actgctgacg 1250
 gctggtcctg aggaaggaca aactgcccag acttgagccc aattaaattt 1300
 tatttttgcg ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415

<211> 224

<212> PRT

<213> Homo sapiens

<400> 415

Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala

1 5 10 15

Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser

20 25 30

Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr

35	40	45
Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro		
50	55	60
Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala		
65	70	75
Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met		
80	85	90
Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu		
95	100	105
Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp		
110	115	120
Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu		
125	130	135
Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro		
140	145	150
Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu		
155	160	165
Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val		
170	175	180
Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln		
185	190	195
Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro		
200	205	210
Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe		
215	220	

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<211> 21

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<213> Artificial Sequence

<220>

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<400> 416

gccatagtca cgacatggat g 21

<210> 417

<211> 18

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<220>

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<400> 417

ggatggccag agctgctg 18

<210> 418

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

aaagtacaag tgtggcctca tcaagc 26

<210> 419

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 419

tctgactcct aagtcaggca ggag 24

<210> 420

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 420

attctctcca cagacagctg gttc 24

<210> 421

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

gtacaagtgt ggctcatca agccctgcc agccaactac ttgcg 46

<210> 422

<211> 1701

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1528

<223> unknown base

<400> 422

gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50

tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100

tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150

cagccagga gctcgtcgc tctctctctc tctctctcac tctccctcc 200

ctctctctct gcctgtccta gtctctagt cctcaaattc ccagtcacct 250

gcaccccttc ctgggacact atgttgttct ccgccctcct gctggaggtg 300

atttgatcc tggctgcaga tgggggtcaa cactggacgt atgagggcc 350

acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400

cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgacctgat 450
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500
ggacctgcac aacaatggcc acacagtga actctctctg ccctctaccc 550
tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600
cactggggtc agaaaggatc cccagggggg tcagaacacc agatcaacag 650
tgaagccaca ttgcagagc tccacattgt acattatgac tctgattcct 700
atgacagctt gagtgaggct gctgagaggc ctcaggcct ggctgtcctg 750
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850
ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc 900
cgctacaatg gctcgtcac aactccccct tgctaccaga gtgtgctctg 950
gacagttttt tatagaaggt cccagatttc aatggaacag ctggaaaagc 1000
ttcaggggac attgttctcc acagaagagg agccctctaa gcttctggta 1050
cagaactacc gagcccttca gcctctcaat cagcgcattg tctttgcttc 1100
tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150
gtgtaggaat ctgggttggc tgtctctgcc ttctcttggc tgtttatttc 1200
attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtggt 1250
cttcacctca gcacaagcca cgactgagge ataaattcct tctcagatac 1300
catggatgtg gatgacttcc ctctatgcct atcaggaagc ctctaaaatg 1350
gggtgtagga tctggccaga aacactgtag gagtagtaag cagatgtcct 1400
ccttccccctg gacatctctt agagaggaat ggaccaggc tgcattcca 1450
ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500

gaaatcgctg tgttgtaat gcagaganca aactctgttt agttgcaggg 1550

gaagtttggg atatacccca aagtcctcta cccctcact ttatggccc 1600

ttccctaga tatactgcgg gatctctct taggataaag agttgctgtt 1650

gaagttgtat attttgatc aatatattg gaaattaaag ttctgactt 1700

t 1701

<210> 423

<211> 337

<212> PRT

<213> Homo sapiens

<400> 423

Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala

1 5 10 15

Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln

20 25 30

Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln

35 40 45

Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp

50 55 60

Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu

65 70 75

Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

80 85 90

Pro Ser Thr Leu Tyr Leu Gly Gly Leu Pro Arg Lys Tyr Val Ala

95 100 105

Ala Gln Leu His Leu His Trp Gly Gln Lys Gly Ser Pro Gly Gly

110 115 120

Ser Glu His Gln Ile Asn Ser Glu Ala Thr Phe Ala Glu Leu His

125 130 135

Ile Val His Tyr Asp Ser Asp Ser Tyr Asp Ser Leu Ser Glu Ala
140 145 150

Ala Glu Arg Pro Gln Gly Leu Ala Val Leu Gly Ile Leu Ile Glu
155 160 165

Val Gly Glu Thr Lys Asn Ile Ala Tyr Glu His Ile Leu Ser His
170 175 180

Leu His Glu Val Arg His Lys Asp Gln Lys Thr Ser Val Pro Pro
185 190 195

Phe Asn Leu Arg Glu Leu Leu Pro Lys Gln Leu Gly Gln Tyr Phe
200 205 210

Arg Tyr Asn Gly Ser Leu Thr Thr Pro Pro Cys Tyr Gln Ser Val
215 220 225

Leu Trp Thr Val Phe Tyr Arg Arg Ser Gln Ile Ser Met Glu Gln
230 235 240

Leu Glu Lys Leu Gln Gly Thr Leu Phe Ser Thr Glu Glu Glu Pro
245 250 255

Ser Lys Leu Leu Val Gln Asn Tyr Arg Ala Leu Gln Pro Leu Asn
260 265 270

Gln Arg Met Val Phe Ala Ser Phe Ile Gln Ala Gly Ser Ser Tyr
275 280 285

Thr Thr Gly Glu Met Leu Ser Leu Gly Val Gly Ile Leu Val Gly
290 295 300

Cys Leu Cys Leu Leu Leu Ala Val Tyr Phe Ile Ala Arg Lys Ile
305 310 315

Arg Lys Lys Arg Leu Glu Asn Arg Lys Ser Val Val Phe Thr Ser
320 325 330

Ala Gln Ala Thr Thr Glu Ala
335

<210> 424

<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 424
gtaaagtcgc tggccagc 18

<210> 425
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 425
cccgatctgc ctgctgta 18

<210> 426
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 426
ctgcactgta tggccattat tgtg 24

<210> 427
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 427
cagaaacca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428

<211> 1073

<212> DNA

<213> Homo sapiens

<400> 428

aattttcac cagagtaaacc ttgagaaacc aactggacct tgagtattgt 50

acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100

gattctactg tttgtcttc taggatcaac tcggtcatta ccacagctca 150

aacctgcttt gggactccct cccacaaaac tggctccgga tcaggaaca 200

ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250

accattaaca cagatgtc cactggggcc agatctgcat ctgttaaacc 300

ctgctgcagg aatgacacct ggtaccaga cccaccatt gacctggga 350

gggttgaatg tacaacagca actgcacca catgtgttac caattttgt 400

cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450

aaatcttcac gacctcatc atccattcct tgtcccggg aggcacctg 500

cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttc 550

agcaggagga gcaggtgtaa atcctgccac ccagggaacc ccagcaggcc 600

gcctccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650

gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc 700

agcaaatgga attcagtaag ctgtttcaaa tttttcaac taagctgct 750

cgaatttggg gatacatgtg aatctttatc attgattata ttatggaata 800

gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850

gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900

cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950

tatgctgcct ggatgatatg catattaaaa catatttga aaactggaaa 1000

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050

aaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429

<211> 209

<212> PRT

<213> Homo sapiens

<400> 429

Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg

1 5 10 15

Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys

20 25 30

Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn

35 40 45

Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu

50 55 60

Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met

65 70 75

Thr Pro Gly Thr Gln Thr His Pro Leu Thr Leu Gly Gly Leu Asn

80 85 90

Val Gln Gln Gln Leu His Pro His Val Leu Pro Ile Phe Val Thr

95 100 105

Gln Leu Gly Ala Gln Gly Thr Ile Leu Ser Ser Glu Glu Leu Pro

110 115 120

Gln Ile Phe Thr Ser Leu Ile Ile His Ser Leu Phe Pro Gly Gly

125 130 135

Ile Leu Pro Thr Ser Gln Ala Gly Ala Asn Pro Asp Val Gln Asp

140 145 150

Gly Ser Leu Pro Ala Gly Gly Ala Gly Val Asn Pro Ala Thr Gln

155	160	165
Gly Thr Pro Ala Gly Arg Leu Pro Thr Pro Ser Gly Thr Asp Asp		
170	175	180
Asp Phe Ala Val Thr Thr Pro Ala Gly Ile Gln Arg Ser Thr His		
185	190	195
Ala Ile Glu Glu Ala Thr Thr Glu Ser Ala Asn Gly Ile Gln		
200	205	

<210> 430

<211> 1257

<212> DNA

<213> Homo Sapien

<400> 430

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cggagcgcgg cggagccaga cgctgaccac gttcctctcc tcggtctcct 100

ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150

gccccgccgc ctccccgcag cggtccgcg gcctctgct gctcctgctg 200

ctgcagctgc ccgcgccgc gagcgcctct gagatcccca aggggaagca 250

aaaggcgcag ctccggcaga gggagggtgt ggacctgtat aatggaatgt 300

gcttacaagg gccagcagga gtcctggtc gagacgggag ccctggggcc 350

aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400

agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacacca 450

actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500

aaaattgcgg agtgtacatt taaaagatg cgttcaaata gtgtctaaag 550

agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600

agcgttggtg ttacacattc aatggagctg aatgttcagg acctcttccc 650

attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700
 aattaatatt catcgactt cttctgtgga aggactttgt gaaggaattg 750
 gtgctggatt agtggatgtt gctatctggg ttggcacttg ttcagattac 800
 ccaaagagg atgcttctac tggatggaat tcagttctc gcacattat 850
 tgaagaacta ccaaataaa tgcttaatt ttcatttgc acctctttt 900
 ttattatgcc ttggaatggt tcacttaaata gacatttaa ataagttat 950
 gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagt 1000
 tgattcaca ctgttttaa atctagcatt attcatttg ctcaatcaa 1050
 aagtggttc aatatattt ttagttggtt agaatactt ctcatagtc 1100
 acattctctc aacctataat ttggaatatt gttgtggtct ttgttttt 1150
 ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200
 aatttgtaa tgtaagaat ttttttata tctgttaaata aaaaattatt 1250
 tccaaca 1257

<210> 431
 <211> 243
 <212> PRT
 <213> Homo Sapien

<400> 431
 Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
 1 5 10 15
 Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
 20 25 30
 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
 35 40 45
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
 50 55 60

Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
65 70 75

Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90

Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
95 100 105

Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
110 115 120

Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
140 145 150

Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
155 160 165

Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
170 175 180

Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
185 190 195

Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
200 205 210

Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
215 220 225

Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
230 235 240

Leu Pro Lys

<210> 432

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 432

aggacttgcc ctcaggaa 18

<210> 433

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 433

cgcaggacag ttgtgaaaat a 21

<210> 434

<211> 21

<212> DNA

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<220>

<223> Synthetic oligonucleotide probe

<400> 434

atgacgctcg tccaaggcca c 21

<210> 435

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<400> 435

cccacctgta ccaccatgt 19

<210> 436

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<400> 436

actccaggca ccatctgttc tccc 24

<210> 437

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<220>

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<400> 437

aagggtggc attcaagtc 19

<210> 438

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

tgacctggca aaggaagaa 19

<210> 439

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439

cagccaccct ccagtccaag g 21

<210> 440

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

gggtcgtgtt ttggagaga 19

<210> 441

<211> 20

<212> DNA

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<400> 441

ctggccctca gacaccaat 20

<210> 442

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 442

tctccatca cttcccctag ctcca 25

<210> 443

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 443

ctggcaggag ttaaagttcc aaga 24

<210> 444

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 444

aaaggacacc gggatgtg 18

<210> 445

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 445

agcgtacact ctctccaggc aaccag 26

<210> 446

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 446

caattctgga tgaggtggta ga 22

<210> 447

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 447

caggactgag cgcttggtta 20

<210> 448

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 448

caaagcgcca agtaccggac c 21

<210> 449

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

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<400> 449

ccagacctca gccaggaa 18

<210> 450

<211> 18

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<223> Synthetic oligonucleotide probe

<400> 450

ccctagctga ccccttca 18

<210> 451

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 451

tctgacaagc agttttctga atc 23

<210> 452

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 452

ctctccccct ccccttctct ttgttt 26

<210> 453

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 453

ctctggtgcc cacagtga 18

<210> 454

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 454

ccatgcctgc tcagccaaga a 21

<210> 455

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 455

caggaaatct ggaaacctac agt 23

<210> 456

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 456

ccttgaaaag gacccagttt 20

<210> 457

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 457

atgagtcgca cctgctgttc cc 22

<210> 458

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tagcagctgc ccttggtta 18

<210> 459

<211> 22

<212> DNA

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<400> 459

aacagcaggt gcgactcatc ta 22

<210> 460

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 460

tgctaggcga cgacaccag acc 23

<210> 461

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 461

tggacacgtg gcagtgga 18

<210> 462

<211> 19

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<223> Synthetic oligonucleotide probe

<400> 462

tcatggtctc gtccattc 19

<210> 463

<211> 27

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<210> 464

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ccggcatcct tggagtag 18

<210> 465

<211> 20

<212> DNA

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<220>

<223> Synthetic oligonucleotide probe

<400> 465

tccccattag cacaggagta 20

<210> 466

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 466

aggetcttgc ctgtcctgct gct 23

<210> 467

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 467

gcccagagtc ccacttgt 18

<210> 468

<211> 19

<212> DNA

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<220>

<223> Synthetic oligonucleotide probe

<400> 468

actgctccgc ctactacga 19

<210> 469

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 469

aggcatcctc gccgtcctca 20

<210> 470

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 470

aaggccaagg tgagtccat 19

<210> 471

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 471

cgagtgtgtg cgaaacctaa 20

<210> 472

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 472

tcagggtcta catcagcctc ctgc 24

<210> 473

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 473

aaggccaagg tgagtccat 19

<210> 474

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 474

cctactgagg agccctatgc 20

<210> 475

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 475

tccaggtgga cccacttca gg 22

<210> 476

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 476

gggaggctta taggccaat ctgg 24

<210> 477

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 477

ggcttcagca gcacgtgtga agtcgaagtc gcagtcacag atatcaatga 50